proteoglycan, used for, e.g. obtaining compounds for
                    reducing **atherosclerosis**.
DERWENT CLASS: B04 D16 S03
INVENTOR(S):   BOREN, J O S; INNERARITY, T L; BOREN, J; INNERARITY, T
PATENT ASSIGNEE(S): (REGC) UNIV CALIFORNIA; (BORE-I) BOREN J; (INNE-I)
                    INNERARITY T
COUNTRY COUNT: 85
PATENT INFORMATION:

      PATENT NO   KIND DATE   WEEK   LA PG

      WO 9946598   A1 19990916 (199946)* EN   69
         RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL
             OA PT SD SE SL SZ UG ZW
          W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GD
             GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV
             MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT
             UA UG UZ VN YU ZW
      AU 9929842   A 19990927 (200006)
      EP 1062512   A1 20001227 (200102)   EN
          R: AT BE CH DE FR GB IE IT LI NL
      US 2001024797 A1 20010927 (200159)
      US 2001029027 A1 20011011 (200162)
      AU 760794   B 20030522 (200338)
      US 6579682   B1 20030617 (200341)

APPLICATION DETAILS:

      PATENT NO   KIND   APPLICATION   DATE

      WO 9946598   A1   WO 1999-US4805   19990305
      AU 9929842   A   AU 1999-29842   19990305
      EP 1062512   A1   EP 1999-911123   19990305
                                          WO 1999-US4805   19990305
      US 2001024797 A1 Provisional   US 1998-77618P   19980310
                       Div ex   US 1999-265222   19990305
                                          US 2001-823418   20010329
      US 2001029027 A1 Provisional   US 1998-77618P   19980310
                       Div ex   US 1999-265222   19990305
                                          US 2001-822965   20010329
      AU 760794   B   AU 1999-29842   19990305
      US 6579682   B1 Provisional   US 1998-77618P   19980310
                                          US 1999-265222   19990305

FILING DETAILS:

      PATENT NO   KIND   PATENT NO

      AU 9929842   A Based on   WO 9946598
      EP 1062512   A1 Based on   WO 9946598
      AU 760794   B Previous Publ.   AU 9929842
                        Based on   WO 9946598

PRIORITY APPLN. INFO: US 1998-77618P   19980310; US 1999-265222
                      19990305; US 2001-823418   20010329; US
                      2001-822965   20010329
AB   WO   9946598 A UPAB: 19991110

DETAILED DESCRIPTION - A novel method for identifying compounds that affect a **low-density** lipoprotein (**LDL**)-proteoglycan (PG) binding comprises:

(a) incubating a mixture by:

(i) PG;

(ii) **LDL,** and

(iii) a candidate compound, where **LDL** binds to PG to form an **LDL**-PG complex in the absence of the candidate compound, and

(b) determining any difference between the amount of **LDL**-PG complex present in:

(i) the mixture as prepared in (a), and

(ii) an assay mixture comprising the PG and the **LDL** in the absence of the candidate compound.

INDEPENDENT CLAIMS are also included for the following:

(1) an apo-B100 protein comprising a PG receptor mutation in Site B;

(2) an **LDL** particle comprising an apo-B100 protein as in (1);

(3) an antibody composition which binds to an antigenic determinant in an apo-B100 protein as in (1), where the antigenic determinant is not present in the wild-type human apo-B100 protein;

(4) a polynucleotide (PN) encoding an apo-B100 protein as in (1), and

(5) a cell comprising a PN as in (4), and

(6) a non-human animal comprising a PN as in (4).

USE - The method can be used for identifying compounds which disrupt **LDL**-PG binding without inhibiting **LDL** receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or **LDL**-PG binding. They can also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The PNs can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal.

ADVANTAGE - None given.

Dwg.0/6

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           MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT
           UA UG US UZ VN YU ZA ZW
      AU 9943580    A  19991108 (200014)
      EP 1071713    A2 20010131 (200108)  GE
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APPLICATION DETAILS:

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    PATENT NO    KIND                    APPLICATION        DATE
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    DE 19816902   A1                      DE 1998-19816902 19980416
    WO 9954352    A2                      WO 1999-DE1137   19990415
    AU 9943580    A                       AU 1999-43580    19990415
    EP 1071713    A2                      EP 1999-926248   19990415
                                          WO 1999-DE1137   19990415
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FILING DETAILS:

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    PATENT NO    KIND                    PATENT NO
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    AU 9943580    A  Based on            WO 9954352
    EP 1071713    A2 Based on            WO 9954352
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PRIORITY APPLN. INFO: DE 1998-19816902 19980416
AB   DE   19816902 A UPAB: 19991210
      NOVELTY - Phosphorylated polypeptides, SREBP1 (sterol regulatory element
      binding proteins) (I) and SREBP2 (II), comprising 1146 and 1141 amino acid
      sequences, respectively, both fully defined in the specification and their
      allelic variants or derivatives with transcription factor activity, are
      new.
           ACTIVITY - Anti-arteriosclerosis; cerebroprotective; cardiant;
      antidiabetic; antihypertensive; anorectic; nootropic; neuroprotective;
      hepatotropic; antineurodegeneration.
           MECHANISM OF ACTION - **Low density** lipoprotein (
      LDL) receptor stimulator, by binding to the sterol-regulatory
      cis-element in the **LDL** gene promoter, in a cholesterol-
      independent manner. The activity of (I) and (II) is regulated not only by
      the cholesterol content of cells but also by post-translational
      modification (phosphorylation).
           USE - (I) and (II) are used to prevent or treat arteriosclerosis,
      stroke, coronary heart disease, peripheral arterial occlusive disease,
      glucose intolerance, diabetes mellitus, arterial hypertension, adiposity,
      disorders of fat metabolism, genetic hypertriglyceridemia (associated with
      lack of ApoC2), Alzheimer's disease, neurodegeneration and genetic liver
      disaease which are modulated by SREBP responsive genes.
           ADVANTAGE - Phosphorylation significantly increases transcriptional
      activity of SREBP-1 or -2.
      Dwg.0/5

L91 ANSWER 41 OF 42   WPIDS   COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 1996-039954 [04]   WPIDS
DOC. NO. CPI: C1996-013405
TITLE: Compsn. containing oligosaccharide(s) that **bind** to
                        lipoprotein lipase - to prevent its interaction
                        with receptors that would cause cellular uptake of
                        lipoprotein, especially to treat or prevent
                        atherosclerosis.
```

COUNTRY COUNT:        64
PATENT INFORMATION:

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    WO 9533468    A1 19951214 (199604)* EN   32
       RW: AT BE CH DE DK ES FR GB GR IE IT KE LU MC MW NL OA PT SD SE SZ UG
        W: AM AU BB BG BR BY CA CN CZ EE FI GE HU IS JP KE KG KP KR KZ LK LR
           LT LV MD MG MN MW MX NO NZ PL RO RU SD SG SI SK TJ TM TT UA UG US
           UZ VN
    AU 9525609    A  19960104 (199613)
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APPLICATION DETAILS:

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    PATENT NO    KIND                  APPLICATION     DATE
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    WO 9533468    A1                   WO 1995-DK217   19950602
    AU 9525609    A                    AU 1995-25609   19950602
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FILING DETAILS:

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    PATENT NO    KIND                  PATENT NO
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    AU 9525609    A  Based on          WO 9533468
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PRIORITY APPLN. INFO: DK 1994-637   19940606
AB   WO   9533468 A UPAB: 19960129
     Compsn. comprises, apart from carrier or diluent, an oligosaccharide of
     formula (I):dUAp2S(1=>4)-[alpha-DGlcNp2R16R2(1=>4)-X(1=>4)]n-alpha-D-
     GlcNp2R16R2,where dUAp2S = 4-deoxy-alpha-L-threo-hex-4-eno-pyranosyl-
     uronic acid, 2-sulphate; alpha-D-GlcNp = alpha-D-2-deoxy-2-amino-
     glucopyranose; X= Idoap2R2(alpha-L-ido-pyranosyl-uronic acid) or
     beta-D-GlcAp (beta-D-gluco-pyranosyl-uronic acid); R1=H, sulphate or
     acetyl; R2= H or sulphate, and n is an integer of 3-16. (I) can bind to
     lipoprotein lipase (LPL) to inhibit interaction between the
     alpha2-macroglobulin receptor/**low density** lipoprotein
     receptor-related protein (alpha2-MR/LRP) and LPL (or its complex with
     lipoprotein). Such as interaction would result in uptake of lipoprotein by
     mammalian cells.
        USE - (I) are used to treat or prevent diseases involving interaction
     between alpha2-MR/LRP (especially when expressed on smooth muscle cells or
     macrophages) and LPL (or its complex with lipoprotein), specifically
     atherosclerosis.(I) is administered at 1-100 mg/kg, given by injection,
     orally, nasally or rectally.
        ADVANTAGE - (I) lock the anticoagulant activity of heparin.
     Dwg.0/3

L91 ANSWER 42 OF 42 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 1991-353525 [48]   WPIDS
CROSS REFERENCE: 1989-356359 [48]; 1998-192802 [17]; 1999-539543 [45];
                        1999-632641 [52]
DOC. NO. CPI: C1991-152440
TITLE: Synthetic peptide(s) comprising amphiphilic domain of
                        apoA-I - used to diagnose vascular injury or disease or
                        inhibit **binding** of **low**
                        density lipoprotein to vascular walls
                        in treating **atherosclerosis**.
```

AB   WO   9116919 A UPAB: 19991221
     Peptides and their analogues which comprise the following amino acid
     sequences are new.
          Tyr-Lys-Leu-Ala-Leu -Glu-Ala-Ala-Arg-Leu-Leu-Ala -Asp-Ala-Glu-Gly-Ala
     Lys; Tyr-Lys-Leu-Ala-Glu-Ala -Ala-Arg-Leu-Leu-Ala-Asn-Ala
     -Glu-Gly-Ala-Lys; Tyr-Arg-Ala-Leu-Val-Asp -Tyr-Leu-Lys-Phe-Val-Thr-Gln-
     Leu; Tyr-Arg-Ala-Leu -Val-Asp-Thr-Leu-Lys; Tyr-Ala-Lys-Phe-Arg-Glu-Thr
     -Leu-Glu-Asp Thr-Arg-Asp-Arg-Met-Tyr; Tyr-Ala-Ala-Leu-Asp
     -Leu-Asn-Ala-Val-Ala-Asn-Lys-Ile -Ala-Asp-Phe-Glu-Leu;
     Tyr-Arg-Ala-Leu-Val-Asp -Thr-Leu-Lys-Phe-Val-Thr-Glu -Gln-Ala-Lys-Gly-Ala;
     and Tyr-Arg-Ala-Leu -Val-Asp-Thr-Glu-Phe-Lys-Val-Lys-Gln
     -Glu-Ala-Gly-Ala-Lys
          The peptides may comprise an amphiphillic domain of apolipoprotein
     A-I and have a net charge of -2 or greater; they are soluble in water and
     plasma. Also claimed are peptides (again with a net charge of at least
     -2), which are derived from a vascular-associated protein such as elastin.
     The peptide may also contain a radioactive label which can be 131I, 125I,
     111In, 99mTc, 203Pb, 198Hg, 97Ru or 201Tc. Alternatively the label is a
     paramagnetic contrast agent.
          USE/ADVANTAGE - (I) have an affinity for and a tendency to accumulate
     at a site of vascular injury. They can be used to diagnose vascular injury
     or disease or to inhibit the binding of **LDL** to vascular walls in
     the treatment of atherosclerosis. Administration may be oral or by
     arterial or venous injection. For diagnostic purposes, dosage is 0.5-1
     mg/i.v. or 5-100 mg orally. For treatment of vascular disease, dosage is
     5-100 mg i.v. or i.m.
     Dwg.0/8

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FILE 'HOME' ENTERED AT 15:58:38 ON 15 MAR 2004

=>

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

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March 12, 2004, 19:55:37 ; Search time 8134.53 Seconds
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Fgapop 6.0 , Fgapext 7.0
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Maximum Match 100%
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6: em_estpl:*
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8: em_htc:*
9: gb_est1:*
10: gb_est2:*
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12: gb_est3:*
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have
score greater than or equal to the score of the result being p...
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Descripti
1	1309	45.9	996	13	BU174966	BU174966
2	1270	44.6	921	13	BQ671165	BQ671165
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6	1217	42.7	707	10	BE746961	BE746961
7	1211	42.5	743	10	BF058118	BF058118
8	1194	41.9	680	10	BE675122	BE675122
9	1189	41.7	683	10	BE857956	BE857956
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25	988	34.7	600	12	BI987692	BI987692
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ALIGNMENTS

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REFERENCE   1 (bases 1 to 996)

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475 GGCAAACCAGCCCTACCTGGGCGCCGACGGCGACCCCTTTGGCTGTCCTCCGGGC

454 GluLysProSerAspProValGluTrpProValThrArgValMetAspValAlaGluTyrPheT
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474 AlaGlyPheProGlyGlnAlaThrAlaPheGluGlnGlnIleAspGlyGlyLysS
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595 GCTGGATTCCCGGAGCAAGCAGCAGCGCTTTCCAGAACACAGAAAATTGATGGCAAAT

493 uLeuLeuMetGlnArgThrAspValArgThrGlyLeuSerIleArgGlyLeuGlyPro
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655 GCTGCTCATGCAGCGCACAAATGTCCACCGGCCTGTCCATCCGCCTCGGGCCA

513 uLysIleTyrGluHisHisIleLysValLeuGlnGlyHisPheGluAspAsp
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775 CGATGGCCTTCTT 787

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  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection
  TITLE   Unpublished (1999)
  JOURNAL
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information c
            found through the I.M.A.G.E. Consortium/LLNL at:
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                     /note="Organ: salivary gland; Vector: pOTB7; Sit
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using
                     following 5' adaptor: GGCACGAG(G). Library cons
                     by Ling Hong in the laboratory of Gerald M. Rubi
                     (University of California, Berkeley) using ZAP-
                     synthesis kit (Stratagene) and Superscript II RT
                     Technologies). Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:

C http://mgc.nci.nih.gov/.
al Institutes of Health, Mammalian Gene Collection (MGC)
ished (1999)
t: Robert Strausberg, Ph.D.
cgapbs-r@mail.nih.gov
Procurement: ATCC
Library Preparation: Rubin Laboratory
Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Sequencing by: Agencourt Bioscience Corporation
distribution: MGC clone distribution information can be
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                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Library constructed
                     by Ling Hong in the laboratory of Gerald M. Rubin
                     (University of California, Berkeley) using ZAP-cDNA
                     synthesis kit (Stratagene) and Superscript II RT (Life
                     Technologies). Note: this is a NIH_MGC Library."

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              13   Gaps: 1

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TTGGCTGCTGCCCCGCCGGGGACAGGCCCGGACGGCCGCCGCCGGCCCGCAGCGCCGC 120

SerArgSerLysArgGlyGlyGluGluAspGluValLeuGluValLysGluGluGluAsp 333
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ProAlaProGlySerGlyLeuThrArgGlnInValPheSerMetAlaAlaMetAsnLysGluGlu 413
|||||||||||||||||||||||||||||||||||||||||||||||||||
CCAGCCCCGGGCAGCGGCACCCGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAA 414

GlyThrAlaSerValAlaThrGlyTyrProSerProAspSerProSerProValProLeuProPro 433
|||||||||||||||||||||||||||||

SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom
REFERENCE   1 (bases 1 to 828)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: DCTD/DTP
              cDNA Library Preparation: Ling Hong/Rubin Laboratory
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information
              found through the I.M.A.G.E. Consortium/LLNL at: image.]
              Plate: LLCM801   row: o column: 11
              High quality sequence stop: 729.
FEATURES   Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:3944674"
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                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI
                     EcoRI; cDNA made by oligo-dT priming. Directi
                     cloned into EcoRI/XhoI sites using the followi
                     adaptor: GGCACGAG(G). Size-selected >500bp fo
                     insert size 1.8kb. Library constructed by Lin
                     the laboratory of Gerald M. Rubin (University o
                     California, Berkeley) using ZAP-cDNA synthesi
                     (Stratagene) and Superscript II RT (Life Techno
ORIGIN

Alignment Scores:
Pred. No.:   3.36e-27   Length: 828
Score: 1241.50   Matches: 251
Percent Similarity: 95.49%   Conservative: 3
Best Local Similarity: 94.36%   Mismatches: 9
DB: 43.56%   Indels: 5
                      10   Gaps: 2

US-09-976-740-43 (1-538) x BE794500 (1-828)

Qy   261 SerGlyGlyAlaGlyGlyArgLeuThrArgGlyValGlnGlyLeuLeuGl
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   3 AGCGGCGGCGCGGGCGGGTCGCCTAACGCGGCCGGTGCA---GGGCTGCTCGGAC

Qy   281 AlaAlaAlaArgGlyArgLeuArgArgGlyThrArgLeuGlyAlaAlaLeuAlaLeuPrc
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   60 GCGGCGGCTCGAGCCCGTCGGAGCGCACCCGTTCGGAGCGCTTGGCGCTGCCC

Qy   301 AspArgProGlyArgAlaProProAlaAlaSerAlaArgProSerArgSerLys
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   120 GACAGGCCCGACGCGGCCCGCCGCCCGGCGCCCAGCGCCCCGCCCGTCGCAGCAAC

Qy   321 GlyGluGluArgValLeuGluLysGluGluGluSerGluGluAspAspAsnProGlu
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   180 GGAGAAGAGGCAGTACTTGAGAAAGAAGAAGAGGAAGAAGATGATGAAGATGAA

Qy   341 GluGluAspAspValSerGluGluValProGluSerGluArgProGluProAlaGly
          |||||||||||||||||||||||||||||||||||||||||||||
Db   240 GAAGATGATGTGTCAGAGGCTCGAAGTGCCCGAGAGTGACCGTCCTGCAGGT

Qy   361 HisHisGlnLeuAsnGlyValArgGlyProGlnSerAlaLysGluArgValLys
          |||||||||||||||||||||||||||||||||||||||||||
Db   300 CACCACCCAGCTTAACGGCGACGCGGGAACCTCAGCGTGCCAAGGAGGAGGGTCAAC

Qy   381 ThrProCysGlyProHisGlnGlyGlnAspGlnGlyArgGlyArgGlyProAlaProGly

---

ty: 5.59e-28   Length: 921
arity: 93.98%   Matches: 247
        92.86%   Conservative: 3
        44.56%   Mismatches: 12
        13   Indels: 4
                         Gaps: 1

(1-538) x BQ671165 (1-921)

nGlyLeuGluGluGluAlaGluAlaAlaArgGlyArgGluArgThrArgLeuGly 293
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aLeuAlaLeuProArgGlyArgAspArgProGlyArgAlaProProAlaAlaSerAlaArg 313
GCTTGCGCTGCCCCGCGGGGACAGGCCCGACGCGGCCCGCCGCCCAGCGCCCGC 120

oSerArgSerLysArgGlyGlyGlyGluGluArgValLeuGluLysGluGluGluSerGluGluAsp 333
GTCTCGCAGCAAGAGAGCGTGGAGAAGAGGCGAGTACTTGAGAAAGAAGAAGAGGAAGAGAT 180

pAspGluAspAspValSerGluGluAspAspValSerGluGluValProGluSer 353
T-----GATGAAGATGAAGAAGATGATGTGTCAGAGGCTCGAAGTGCCCGAGAGT 234

pArgProAlaGlyHisHisGlnLeuAsnGlyValArgGlyProGlnSerAla 373
CCGTCCTGCAGGTGCCCAGCCACCACCAGCTTAACGGCGAGCGGGGGACCTCAGAGTGCC 294

sGluArgValLysThrProCysGlyProHisGlnGlyGlnAspGlnGlyArg 393
GGAGCGGGTCAAGGAGGTCGAACCCCTGCGAGACCGCCAGGATGAAGGGCGG 354

yProAlaProGlySerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGlu 413
GCCAGCCCCGGGAGCGGCGCACCCGCCCAGGTGTTCTCATGGCAGCCATGAACAAGGAA 414

yGlyThrAlaSerValAlaThrGlyThrGlyProSerProValProLeuProPro 433
GGGAACAGCTTCTGTTGCCACCGGCCCAGACTCCCCGTCCCCGTGCCTTTGCCCCCA 474

yLysProAlaLeuProGlyAlaAspGlyThrProPheGlyCysProProGlyArgLys 453
CAAACCAGCCCCTACCTGGGCGCAGCGGACCCCCTTTGGCTGTCCTCCCGGGGCGCAAA 534

uLysProSerArgAspProValGluTrpThrArgValMetAspValValGluTyrPheThrGlu 473
GAAGCCATCTGATCCCGTCAAGTGGACCGTGAGTGGATGTCGTCGAATATTTTACTGAG 594

aGlyPheProGluGlnAlaThrAlaPheGlnGlnGluGlnGluIleAspGlyLysSerLeu 493
TGGATTCCCGGAGCAGGCGACAGCTTTCCCAGAGCAGGAAATTGATGGCAAATCTTTG 654

uLeuMetGlnArgThrArgAspValLeuThrGlyLeuSerIleArgGlyLeuGlyProAlaLeu 513
GCTCATGCAGCGCGGGATGTGCTTCCCGGGCGTGTTCATCGCCCTCGGGGCCAACCCTG 714

sIleTyrGluHisHisIleLysValLeuGln-GlnGlyHisPheGlu-AspAspAspP 533
ATTCTACGATCACCAGATCAAGGGGCTTTCCGCAGGGCCCCTTTGAGGGGTGATGACC 774

AspGlyPheLeu 537
::::||||||||
GAGGGGCTTCTTA 788

4500
90248F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944674 5',
sequence.
4500   828 bp   mRNA   linear   EST 20-SEP-2000
4500.1 GI:10215698

ORIGIN   (Stratagene) and Superscript II RT (Life Technol

Alignment Scores:
Pred. No.:   9.81e-27   Length: 1109
Score: 1229.00   Matches: 229
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 43.12%   Indels: 0
DB: Gaps: 0

US-09-976-740-43 (1-538) x BE270805 (1-1109)

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Qy  310 AlaSerAlaArgProSerArgLysArgGlyGluGluArgValLeuGlu!
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3 GCCAGCGCCCCGCCCGTCTCGCAGCAAGAGAGGTGGAAGAGAGCGAGTACTTGAG!

Qy  330 GluGluGluAspAspAspGluAspGluAspGluAspAspValSerGluGly!
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   63 GAGGAAGAAGATGATGATGAAGATGAAGATGAAGATGATGTCAGAGGGC!

Qy  350 ValProGluSerAspArgProAlaGlyAlaGlnHisHisGlnLeuAsnGlyGlu!
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Db  123 GTGCCCGAGAGTGACCGTCCTGCAGGTGCCCAGCACCACCAGCTTAACGGCGAG!

Qy  370 ProGlnSerAlaLysArgValLysGluTrpThrProCysGlyProHisGln!
        ||||||||||||||||
Db  183 CCTCAGAGTGCCAAGGAGGAGGTCAAGGAGTGGACCCCCTGCCGACCCGCACCAG!

Qy  390 AspGluGlyArgGlyProAlaProGlySerGlyThrArgGlnValPheSerMet!
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db  243 GATGAAGGGCGGGGGCCCAGCCCCGGGAGCGGCACCCGGCAGGTGTTCTCCATG!

Qy  410 MetAsnLysGluGlyGlyThrAlaSerValAlaThrGlyProSerProSer!
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  303 ATGAACAAGGAAGGGGGAACAGCTTCGTGTTGCCACGGGCCAGACTCCCGTCC!

Qy  430 ProLeuProProGlyLysProAlaLeuProGlyAlaAspGlyThrProPheGly!
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db  363 CCTTTGCCCCCAGGCAAACCAGCCTTACCTGGGGCCGACGGGACCCCCTTTGGC!

Qy  450 ProGlyArgLysGlyLysProSerArgAspProValGluTrpThrValMetAspVal!
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Db  423 CCCGGGCGCAAAGAAGAGAAGCCATCTGATCCCGTCGAGTGGACCGTGATGGATGTC!

Qy  470 TyrPheThrGluAlaGlyPheProGluGlnAlaThrAlaPheGlnGluGlnGlu!
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  483 TATTTTACTGAGGCTGGATTCCCGGAGCAGGCGACAGCTTTCCAAGAGCAGGAA!

Qy  490 GlyLysSerLeuLeuLeuMetGlnArgThrArgAspValLeuThrGlyLeuSerIle!
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  543 GGCAAATCTTTGCTGCTCATGCAGCGCACAGATGTGCTTACCGGCCTGTCCATC!

Qy  510 GlyProAlaLeuIleTyrGluHisHisIleLysValLeuGlnGlyHisHisIle!
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  603 GGGCCAGCCCTGAAAATCTACGAGCACCACCATCAAGGTGCTTCAGCAAGGCCAC!

Qy  530 AspAspAspProAspGlyPheLeuGly  538
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Db  663 GATGATGACCCCGATGGCTTCTTAGGC  689
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RESULT 5
BF058975
LOCUS   BF058975   704 bp   mRNA   linear   EST :
DEFINITION 7k36f08.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3!
            similar to TR:O76866 O76866 EG:100G10.6 PROTEIN. [1] ;co!
            element MER22 repetitive element ;, mRNA sequence.
ACCESSION   BF058975
VERSION   BF058975.1 GI:11812871
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute!

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CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGAACAGCTTCTGTTGCC 479

GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGly 440
|||||||||||||||||||||||||||||||||||||||||||||||||
GGGCCAGACTCCCCGTCCCCGTGCCTTTGCCCCCAGGCAAACCAGCCTTACCTGGG 539

AspGlyThrProPheGlyProGlyCysProGlyArgLysGluLysProSerArgAspProVal 460
|||||||||||||||||||||||||||||||||||||||||||
GACGGGACCCCCTTGGCTGCTCCCCGGGCGCAAAGAAGAAGCCATCTGATCCCGTC 599

TrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGluGlnAla 480
||||||||||||||||||||||||||||||||||||||||||||||
TGGACCGTGATGGATGTCGTCGAATATTTTACTGAGGCTGGATTCCCGGAGCAGGCG 659

AlaPheGlnGluGln-GluIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAs 500
:::|||||||||||||||||||||||||||||||||||
AGTTTTCAAGAGCAGGGGAAATTGATGGCAAATCTTTGCTGTC-ATGCAGCGCACAGA 718

IleLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuIleTyrGluHisHisIl 520
||||||||||||||||||||:::|||||||||
GCTCACGG--CTTGTCATTCGGCTCGGGCCAGCCTGAAAATTAAGAGCACACAT-- 774

sValLeuGlnGln 525
:|||||||||
GGTGCTTCAGCAG 789

805   1109 bp   mRNA   linear   EST 13-JUL-2000
3804F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2966449 5',
sequence.
805
805.1   GI:9144449

sapiens (human)
sapiens
yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
lia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ases 1 to 1109)
GC http://mgc.nci.nih.gov/.
nal Institutes of Health, Mammalian Gene Collection (MGC)
lished (1999)
ct: Robert Strausberg, Ph.D.
: cgapbs-r@mail.nih.gov
e Procurement: Louis M. Staudt, M.D., Ph.D.
Library Preparation: Ling Hong/Rubin Laboratory
Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Sequencing by: Incyte Genomics, Inc.
ne distribution MGC clone distribution information can be
l through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
: LLCM69   row: h column: 02
quality sequence stop: 749.
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/clone="IMAGE:2966449"
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EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit

ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAla 419
||||||||||||||||||||||||||||||||||||||||||||||||||
CCCTGCGACCGCACCAGGGCCAGGATGAAGGGCGGGGCCAGCCCCGGGCAGCGGC

alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
bases 1 to 704)
CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
onal Cancer Institute, Cancer Genome Anatomy Project (CGAP),
r Gene Index
blished (1997)
act: Robert Strausberg, Ph.D
l: cgapbs-r@mail.nih.gov .
ue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
mmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
es, Ph.D. cDNA Library Arrayed by: Christa Prange, The
A.G.E. Consortium DNA Sequencing by: Washington University
me Sequencing Center
ne distribution: NCI-CGAP clone distribution information can be
d through the I.M.A.G.E. Consortium/LLNL, send email to:
@image.llnl.gov
primer: -40UP from Gibco
quality sequence stop: 495.
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                /clone_lib="NCI_CGAP_Ov18"
                /note="Organ: ovary; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGGAGCGGCCGCGGACCATTTTTTTTTTTTTTTTTT 3'];
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "

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        9.3e-27        Length:        704
        1224.00        Matches:       231
ty:     99.15%         Conservative:  1
arity:  98.72%         Mismatches:    2
        42.95%         Indels:        0
        10             Gaps:          0
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(1-538) x BF058975 (1-704)

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     CCGGTGCAAGGGGCTGCTGGAGGAGGAGGAGGCGGGCGCGTCTCGAGGCCGTCTGGAGGCCACC 62

     gLeuGlyAlaLeuAlaLeuProArgGlyArgAspArgProGlyArgGlyAlaProProAlaAla 310
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     rAlaArgProSerArgSerLysArgGlyGlyGlyGluGluGlnLysArgValLeuGluLysGluGlu 330
      ||||||||||||||||||||||||||||||||||||||||||||||
     CGCCCGCCCCGTCTCGCAGCAAGGCGGTGGAGAAGAGCCAGTACTTGAGAAAGAAGAG 182

     uGluAspAspAspGluAspGluGluAspGluSerGluGlyValSer 350
      ||||||||||||||||||||||||||||||||||||||
     AGAGATGATGAAGAAGATGAAGAAGATGAAGAAGAGATGAGTGTCAGAGGGCTCTGAAGTG 242

     oGluSerAspArgProAlaGlyAlaGlyAlaAlaGlnHisHisHisGlnLeuAsnGlyGluGlyGlyGlyPro 370
      |||||||||||||||||||||||||||||||||||||||||
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     nSerAlaLysGluArgValLysGlyLeuTrpThrProCysGlyValTrpProHisGlnHisGlyGlnAsp 390
      ||||||||||||||||||||||||||||||||||||||||||
     GAGTGCCAAGGAGGAGGGGTCAAGGAGGTGGACCCCTGCGAGACCGACCACCAGGGCCAGGAT 362

     uGlyArgGlyProAlaProGlySerGlyThrArgGlyValPheSerMetAlaAlaMet 410
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Right column:

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Db     363 GAAGGGCGGGGGCCAGCCCCGGGCAGGGGCACCGCCGCCAGGTGTTCTCCATGGC
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Qy     411 AsnLysGluGlyGlyThrAlaSerValAlaThrGlyProAspSerProSerPr
Db     423 AACAAGGAAGGGGGAACAGCTTCTCGTTGCCACCGGGCCAGACTCCCCGTCCCC
Qy     431 LeuProProGlyAlaLeuProGlyAlaAspGlyThrProPheGlyCy
Db     483 TTGCXCCCAGCAAACCAGCCCTACCTGGGGCCGACGGGACCCCNTNGGCTG
Qy     451 GlyArgLysGluLysProSerAspProValGluTrpThrValMetAspValVa
Db     543 GGGCGCAAAGAGAAGCCATCTGATCCCGTCGACGTGGGACCCGTGATGGATGTCGT
Qy     471 PheThrGluAlaGlyPheProGluGlnAlaThrAlaPheGlnGlnGluGluGlnGluI
Db     603 TNTACTGATGCTGGATTCCCGGAGCAGGCAGCGGACTGCTTTCCAAGAGCAGGAAAT
Qy     491 LysSerLeuLeuMetGlnArgThrArgpValLeuThrGly 504
Db     663 AAATCTTTGCTGCTCATGCAGCGCACAGATGTGCTCACCGGG 704
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RESULT 6
BE746961
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LOCUS       BE746961               707 bp    mRNA    linear    EST
DEFINITION  601580088F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:392
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ACCESSION   BE746961
VERSION     BE746961.1  GI:10160953
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho
            1 (bases 1 to 707)
REFERENCE   NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS     National Institutes of Health, Mammalian Gene Collectio
TITLE       Unpublished (1999)
JOURNAL
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLl
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information
            found through the I.M.A.G.E. Consortium/LLNL at: image.
            Plate: LLCM762 row: p column: 22
            High quality sequence stop: 671.
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:3929733"
                     /tissue_type="adenocarcinoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_9"
                     /note="Organ: ovary; Vector: pOTB7; Site 1: Xh
EcoRI; cDNA made by oligo-dT priming. Directi
cloned into EcoRI/XhoI sites using the followi
adaptor: GGCACGAG(G). Size-selected >500bp fo
insert size 1.8kb. Library constructed by Lin
the laboratory of Gerald M. Rubin (University
California, Berkeley) using ZAP-cDNA synthesi
(Stratagene) and Superscript II RT (Life Techn
ORIGIN
```

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Alignment Scores:
Pred. No.:                              1..707
Score:                  1.48e-26        Length:        707
                        1217.00         Matches:       229
Percent Similarity:     99.14%          Conservative:  2
Best Local Similarity:  98.28%          Mismatches:    2
```

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D.,
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M.
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, Th
I.M.A.G.E. Consortium DNA Sequencing by: Washington Unive
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution informat
found through the I.M.A.G.E. Consortium/LLNL, send email
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 495.
1..743

FEATURES   Location/Qualifiers
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                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NCI_CGAP_Ov18"
                /note="Organ: ovary; Vector: pT7T3D-Pac (Pharmac
                modified polylinker; Site 1: Not I; Site 2: Eco
                strand cDNA was primed with a Not I - oligo(dT)
                TGTTACCAATCTGAAGTGGGAGGCGGCCGCGACAATTTTTTTTTTTT
                double-stranded cDNA was ligated to Eco RI adapt
                (Pharmacia), digested with Not I and cloned int
                I and Eco RI sites of the modified pT7T3 vector
                went through one round of normalization, and was
                constructed by Bento Soares and M. Fatima Bonal(

ORIGIN

Alignment Scores:
Pred. No.:   2.3e-26   Length: 743
Score: 1211.00   Matches: 232
Percent Similarity: 94.74%   Conservative: 2
Best Local Similarity: 93.93%   Mismatches: 13
Query Match: 42.49%   Indels: 0
DB: 10   Gaps: 0

US-09-976-740-43 (1-538) x BF058118 (1-743)

Qy 271 GlyArgValGlnGlyLeuLeuGluGluAlaAlaAlaArgGlyArgLeuGlu
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Db   3 GGCCGCGTGCAGGGCTGCTGGAGGAGGAGGCGGCCGGCGCCGTCTGGAG(

Qy 291 ArgLeuGlyAlaAlaLeuAlaLeuProArgGlyAspArgProGlyArgProAlaProPro(
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   63 CGTCTCCGAGCCGCTTGGCGTGCCCCCGGGGACAGGGCCCGGACGGGCCGCGCCG(

Qy 311 SerAlaArgProSerArgSerLysArgGlyGlyGlyGluGluArgValLeuGluLys(
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 123 AGCGCCCCGCCCGTCTCGCAGCAAGCAAGAGGAGTGGAAGAAGCGAGTACTTGAGAAA(

Qy 331 GluGluAspAspAspGluGluGlyAspGluAspGluSerGluGlySer(
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 183 GAAGAAGATGATGATGAAGAATGAAGAATGAAGAAGATGATGTTCAGAGGGCTCT(

Qy 351 ProGluSerAspArgProAlaGlyAlaGlnHisHisGlnLeuAsnGlyLeuArgG(
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 243 CCCGAGAGTGACCGTCCTGCAGTGCCCAGCACCACCAGCTTAACGGCGGAGCGG(

Qy 371 GlnSerAlaLysGluArgValLysGluTrpProThrProCysGlyProHisGlnGlyV(
         ||||||||||||||||||||||||||||||||||||||||||||
Db 303 CAGAGTGCCAAGGAGAGGGTCAAGGAGTGGACCCCCTGCGGACCGCACCAGGGGC(

Qy 391 GluGlyArgGlyProAlaProGlySerGlyThrArgGlnValPheSerProMetAla(
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 363 GAAGGGCGCGGGGGGCCAGCCCCCGGCAGCGCCACCCGCACCCAGGTGTTCTCCATGGCA(

Qy 411 AsnLysGluGlyGlyThrAlaSerValAlaThrGlyTyrProAspSerProSer(
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 423 AACAAGGAAGGGGGAACAGCTTCTGTTGCCACCGGGCCAGACTCCCCGTNCCC(

Qy 431 LeuProProGlyLysProAlaLeuProGlyAlaAspGlyThrProPheGlyCysI(

GlyGlyAlaGlyGlyArgThrArgGlyArgValGlnGlyLeuLeuGluGluGlu 280
|||||||||||||||||||||||||||||||||||||||||||||||||||
GGCGGCGGCCGGCGGTCGCTAACCCGCGCCGGCCGCCGCTGCTGGAGGAGGAG 62

AlaAlaArgGlyArgLeuGlyArgThrArgLeuGlyAlaAlaLeuAlaLeuProArgGly 300
|||||||||||||||||||||||||||||||||||||||||||||||||||
GCGGCTCGAGGCCCGTCTGGAGCGCACCCGTCTCGAGCCGCTTGCGCTGCCCCGCGGG 122

ArgProGlyArgProAlaProProAlaSerAlaAlaArgProSerArgSerLysArgGly 320
|||||||||||||||||||||||||||||||||||||||||||||||||||
AGGCCCGGACGGGCCGCCGCCGCCAGCGCCCCGCCCGTCTCGCAGCAAGCAAGAGGT 182

GluGluArgValLeuGluLysGluGluGluGluGluAspAspAspGluGluAspGlu 340
|||||||||||||||||||||||||||||||||||||||||||||||||||
GAAGAGCGAGTACTTGAGAAAGAAGAAGAGAGAAGATGATGAAGAAGATGAAGAATGAA 242

AspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHis 360
|||||||||||||||||||||||||||||||||||||||||||||||||||
GATGATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCCTGCAGGTGCCCAG 302

HisGlnLeuAsnGlyLeuArgGlyGlnSerAlaLysGluArgValLysGluTrp 380
|||||||||||||||||||||||||||||||||||||||||||||||||||
CACCAGCTTAACGGCGGAGCGGGACCTCAGAGTGCCAAGGAGAGGGTCAAGGAGTGG 362

ProCysGlyProHisGlnGlyValGlnAspGluGlyArgGlyProAlaProGlySerGly 400
|||||||||||||||||||||||||||||||||||||||||||||||||||
CCCTGCGGACCGCACCAGGGCGGGTCCAGGATGAAGGGCGCGGGGGGCCAGCCGCGGC 422

ArgGlnValPheSerProMetAlaAlaAsnLysGluGlyGlyThrAlaSerValAla 420
|||||||||||||||||||||||||||||||||||||||||||||||||||
CGCCAGGTGTTCTCCATGGCAGCAGCCATGAAAGGGAACAAGGAAGGGGGAACAGCTTCTGTTGCC 482

TrpThrValMetAspValValGluTyrProPheThrGluAlaGlyLysProGlnGlnAla 480
|||||||||||||||||||||||||||||||||||||||||||||||||||
TGGACCGTGATGGATGTCGTCGAATATTTTACTGAGGCTGGATTCCCGGAGCAGGCG 662

GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGly 440
|||||||||||||||||||||||||||||||||||||||||||||||||||
GGGCCAGACTCCCCGTCCCGTGCCTTTGCCCCCAGGCAAACCAGCCCTACCTGGG 542

AspGlyThrProPheGlyCysProProGlyArgLysGluLysGluProSerArgAspPro 460
||||||||||||||||||||||||||||||||| ::::
GACGGGACACCCCCCTTTGGCTGTCCTCCCCGGGCGCAAAAGAAGAGCCATCTGATCCCGTC 602

AlaPheGlnGlnGluLeuAspGlyLysSerLeu 493
|||||||:::::||: ::::
GCTTTCCAAAAGCAACAGGAAATCGATTGGCAAATTCTT 701

118   743 bp   mRNA   linear   EST 16-OCT-2000
12.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3477623 3'
ar to TR:O76866 O76866 EG:100G10.6 PROTEIN. [1] ;contains
nt TAR1 repetitive element ;, mRNA sequence.
118
118.1   GI:10812014
sapiens (human)
sapiens
yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ilia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
oases 1 to 743)
GAP http://www.ncbi.nlm.nih.gov/ncicgap.
nal Cancer Institute, Cancer Genome Anatomy Project (CGAP),
; Gene Index
olished (1997)
ict: Robert Strausberg, Ph.D.
L: cgapbs-r@mail.nih.gov

42.70%   Indels: 0
10   Gaps: 0

(1-538) x BE746961 (1-707)

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Best Local Similarity:    99.12%        Mismatches:    1
Query Match:              41.89%        Indels:        0
DB:                       10            Gaps:          0

US-09-976-740-43 (1-538) x BE675122 (1-680)

Qy    271  GlyArgValGlnGlyLeuLeuGluGluGluAlaAlaArgGlyArgLeuGl
Db      3  GGCCGCCTGCGTGCTGCTGGAGGAGGAGGCGGCTCGAGGCCGTCTGGA

Qy    291  ArgLeuGlyAlaLeuAlaLeuProArgGlyAspArgProGlyArgAlaProPr
Db     63  CGTCTCCGAGCGCTTGGCCGCTGCCCCGGGGACAGGCCCGGACAGCGGCCGCC

Qy    311  SerAlaAargProSerArgSerLysArgGlyGlyGluGlyGluArgValLeuGluLy
Db    123  AGCGCCCGCCCGTCTCCGCAGCAAGAGAGGTGGAGAAGAGCGAGTACTTGAGAA

Qy    331  GluGluAspAspAspGluAspGlyGluGlyAspGluAspAspValSerGluGlySe
Db    183  GAAGAAGATGATGATGAAGATGAAGATGAAGATGAAGATGATGTCTCAGAGGGCTC

Qy    351  ProGluSerAspArgProAlaGlyAlaGlnHisHisGlnLeuAsnGlyGluAr
Db    243  CCCGAGAGTGACCGTCTCGCAGGTGCCCAGCACCACCAGCTTAACGGCGAGCG

Qy    371  GlnSerAlaLysGluArgValLysGluTrpThrProCysGlyProHisGlnGl
Db    303  CAGAGTGCCAAGGAGGAGGGTCAAGAGTGACCCCTGCGACCGGACCAGGGG

Qy    391  GluGlyArgGlyProAlaProGlySerGlyThrArgGlnValPheSerMetAl
Db    363  GAAGGGCGGGGGCCAGCCCCGGCAGCGCCACCCGGCCACCCGGTGTTCTCCATGGC

Qy    411  AsnLysGluGlyGlyThrAlaSerValAlaThrGlyProAspSerProSerPr
Db    423  AACAAGGAAGGGGGAACAGCTTCGTTGCCACGGGCACGGCCAGACTCCCCGTCCC

Qy    431  LeuProGlyLysProAlaLeuProGlyAlaAspGlyThrProPheGlyCy
Db    483  TTGCCCCCAGGCAAACCAGCCTACCTGGGCGGCAGCGGCACCCCCTTTGGCTG

Qy    451  GlyArgGluLysProSerAspProValGluTrpProValMetAspValVa
Db    543  GGGCGCAAAGAGAGAAGCCATCTGATCCCGTCGAGTGACCGTGATGGATGTCGT

Qy    471  PheThrGluAlaGlyPheProGluGlnAlaThrAlaPheGlnGluGlnGluLeu
Db    603  TTTACTGAGGCTGGATTCCCGGAGCAGGCGGACAGCTTTCCAAGAGCACGAAAT

Qy    491  LysSerLeuLeuLeuMet  496
Db    663  AAATCTATGCTGCTCATG  680


RESULT 9
BE857956
LOCUS       BE857956         683 bp    mRNA       linear    EST
DEFINITION  7f73a12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA
            IMAGE:3300286 3' similar to TR:O76866 O76866 EG:100G10.6
            [1] ;contains element MER22 repetitive element ;, mRNA s
ACCESSION   BE857956
VERSION     BE857956.1    GI:10372500
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom
            1 (bases 1 to 683)
REFERENCE   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS     National Cancer Institute, Cancer Genome Anatomy Project
TITLE       Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
```

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:YArgLysGluLysProSerAspProValGluTrpThrValMetAspValValGluTyr  470
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:GCGCAAGAGAAGCCATCTGATCCCGTCGAGTGACCGTGATGGATGTCGTCGAATAT  602

eThrGluAlaGlyPheProGluProGlnAlaPheGlnGlnGluGlnGluIleAspGlyGly  490
|||  |||||||||||||||||||||||||||||||:::|||||||||
TACTGAGGCTGGATTCCCGGAGCCGGACCAGCGGCGACGNCTTCCGAGAGCAGGAAATCGATCGC  662

sSerLeuLeuLeuMetGlnArgThrArgAspValLeuThrGlyLeuSerIleArgLeuGly  510
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ATCTTTGCTGCTCATGCAGCGACAGATGTGCTCTCCGCTGTCCATCCTGCTTTGGG  722

oAlaLeuLysIleTyrGlu  517
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AGGCCCTGATATCTACGAG  743

5122                680 bp    mRNA      linear    EST 08-SEP-2000
h07.x1 NCI_CGAP_CLl1 Homo sapiens cDNA clone IMAGE:3293533 3'
lar to TR:Q24191 Q24191 TRANSCRIPTIONAL REPRESSOR PROTEIN.
tains element MER22 repetitive element ;, mRNA sequence.
5122
5122.1  GI:10035663

sapiens (human)
sapiens
ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
bases 1 to 680)
CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
onal Cancer Institute, Cancer Genome Anatomy Project (CGAP),
r Gene Index
blished (1997)
act: Robert Strausberg, Ph.D.
l: cgapbs-r@mail.nih.gov
ue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
, Louis M. Staudt, M.D., Ph.D.
A Library Preparation: M. Bento Soares, Ph.D.
A Library Arrayed by: Greg Lennon, Ph.D.
Sequencing by: Washington University Genome Sequencing Center
ne distribution: NCI-CGAP clone distribution information can be
d through the I.M.A.G.E. Consortium/LLNL, send email to:
@image.llnl.gov
primer: -40UP from Gibco
quality sequence stop: 479.
Location/Qualifiers
1..680
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3293533"
/tissue_type="B-cell, chronic lymphotic leukemia"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_CLl1"
/note=Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGGAGGCGGCCGCATTGCTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

:         Length:     680
          Matches:    224
ty:       Conservative:  1

6.55e-26
1194.00
99.56%
```

```
: cgapds-r@mail.nih.gov
clone is available royalty-free through LLNL ; contact the
Consortium (info@image.llnl.gov) for further information.
rimer: -40UP from Gibco
quality sequence stop: 454.
          Location/Qualifiers
          1..683
          /organism="Homo sapiens"
          /mol_type="mRNA"
          /db_xref="taxon:9606"
          /clone="IMAGE:3300286"
          /lab_host="DH10B"
          /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
          /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
          a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and cloneIDs: Soares NbHSF pool 1:
309384-310919, 323208-325895 Soares Nb2HP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares Nb2HF8-9W pool 1:
758280-760583, 772104-774407 Soares NbHPA pool 1:
304776-306311, 320136-322823, 326280-326663 Soares NbHOT
pool 1: 723720-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Bonaldo."
```

```
                9.15e-26        Length:         683
                1189.00         Matches:        224
y:              99.56%          Conservative:   1
urity:          99.12%          Mismatches:     1
                41.72%          Indels:         0
                10              Gaps:           0

(1-538) x BE857956 (1-683)
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:GAGGAGGAGGCGGCGGCTCGAGGCCGTCTGGAGCGCCACCCGTCTCGGAGCGCTTGCG 62

1ProArgGlyAspArgProGlyArgAlaProProAlaAlaSerAlaArgProSerArg 316
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
:CCCCGCGGGACAGGCCCGGACGGCGCCCGGCCGCCGCCAGCGCCCGTCTCGC 122

1LysArgGlyGlyGluGlnArgValLeuGlyValLeuGluGluGluLysAspAspAspGlu 336
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
AAGAGAGGTGGAGAGAGCCAGTACTTGACGAAAGAAGAGGAAGATGATGATGAA 182

:GluAspGluAspAspValSerGluGlyGlySerGluValProGluSerGluArgPro 356
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
:GAAGATGAAGAAGATGATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCCT 242

1GlyAlaGlnHisHisGlnLeuAsnGlyGluArgGlyGluProGlnSerAlaLysGluArg 376
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
:GGGTGCCCAGCACCACCAGCTTAACGGCAGGCGGGGGACCTCAGAGTGCCAAGGAGAGG 302

1LysGluTrpThrProCysGlyProHisGlyInGlyGlnAspGluGlyArgGlyProAla 396
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
:AAGGAGTGGACCCCCTGCGACCGCACCAGGGCCCAGGATGAAGGGCGGGGCCAGCC 362

:GlyGerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThr 416
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
:GGGCAGCGGCACCCGCCAGGTGTTCTTCCATGGCAGCCATGAACAGGAAGGGGGAACA 422

:SerValAlaThrGlyProAspSerProSerProValProLeuProProGlyLysPro 436
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
:TTCTGTTGCCACCGGGCCAGACTCCCCGTCCCCGTGCCTTTGCCCCCCCAGGCAAACCA 482
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High quality sequence stop: 751.

FEATURES   Location/Qualifiers
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                  /db_xref="taxon:9606"
                  /clone="IMAGE:3917399"
                  /tissue_type="melanotic melanoma"
                  /lab_host="DH10B (phage-resistant)"
                  /clone_lib="NIH_MGC_72"
                  /note="Organ: skin; Vector: pCMV-SPORT6; Site
                  Site 2: SalI; Cloned unidirectionally. Primer
                  Average insert size 2 kb.   Library constructe
                  Technologies."

ORIGIN

Alignment Scores:
Pred. No.:   Length: 774
Score: 4.64e-25   Matches: 243
Percent Similarity: 1166.00   Conservative: 1
Best Local Similarity: 95.31%   Mismatches: 5
Query Match: 94.92%   Indels: 9
DB: 40.91%   Gaps: 2
                       10

US-09-976-740-43 (1-538) x BE891267 (1-774)

Qy   288 GluArgThrArgLeuGlyAlaLeuAlaLeuAlaLeuProArgGlyAspArgProGlyAlaArg
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2 GAGCGGACACCCGTCTCCGAGCCGTTGCGCTGCCCCGGGGGGACCAGGCCCGGGACGCGGACG

Qy   308 ProAlaAlaSerAlaArgProSerArgSerLysArgGlyGlyGluGlyGlyGluGluArgGlyVa
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   62 CCGGCGGCCAGCGCCCGCCCGTCTCGCAGCAGAGAGAGTGGAGAAGAGCGAGT

Qy   328 LysGluGluGluGluAspAspAspGluGluAspGluAspAspGluAspValSe
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   122 AAAGAAGAGGAAGAAGAAGATGATGAGAAGAGAGAAGATGATGAGAAGAGAAGATGATGTC

Qy   348 SerGluValProGluSerArgAspArgProAlaGlyAlaGlnHisHisGlnLeuLeuAs
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   182 TCTGAAGTGCCCGAGAGTGACCGTCCTGCAGTGCCCAGCCACCACCAGCTTAA

Qy   368 ArgGlyProGlnSerAlaLysGluArgValLysGluTrpThrProCysGlyPr
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   242 CGGGGACCTCAGAGTGCCAAGGAGAGGGTCAAGGAGTGGACCCCCCTGCGGACC

Qy   388 GlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThrArgGlnValPh
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GGCCAGGATGAAGGCGGGGGGCAGCCCCGGGCAGCGGCGCACCCGGCCACCCGGCCAGGTGTT

Qy   408 AlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThrGlyProAspSe
         ||||||||||||||||||||||||||||||||| :::||||||||||
Db   361 GCAGCCATGAACAAGGAAGGGGGAACAGCTTCGTTGCCACCGGGCCAGACTC

Qy   428 ProValProLeuProProGlyLysProAlaLeuProGlyAlaAspGlyThrPr
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CCCGTGCCTTTGCCCCCAGCAAACCAGCCCCTACCTGGGGCCGACGGGACCCCC

Qy   448 CysProProGlyArgLysGluLysProSerAspSerProValGluTrpThrValMet
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TGTCCTCCCGGGCGCAAAGAAGAAGCCATCTGATCCCGTCGAGTGGACCGTGAT

Qy   468 ValGlu-TyrPheThrGluAla-GlyPhePro-- -GluGlnAlaThrAlaPhe
         |||||||||||||||||||||||||| :::|||||||||||
Db   541 GTCGAAATATTTTACTGAGGCTTGGATTTCCCGGAGCAAGGCAAGCAGCTTTC

Qy   486 lnGluIleAspGlyLysSerLeuLeuLeu-MetGln-ArgThrAspValLeuTh
         ||||||||||||||| |||||| |||||||||||||||||
Db   601 AGGAAATTGATGGCAAATCTTTGCTGCTCAATGCAGGCGACCAGATGTGCTCA

Qy   505 uSerIleArgLeuGlyProAlaLeuGlyIleTyrGluHisHisIleLysValLe
         ||||||||||||||||||||||||||||| :::|||||||||||||||
Db   661 GTCCATCCGCCTCGGCCAGC-CTGAAAATCTACGAGCACCACCATCAAGGTGC

──── (right column below) ────

         ||||||||||||||||||||||||||||||||||||||||||||||||
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sGlyTyrProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThrArg 402
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nValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThrGly 422
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oAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAlaAsp 442
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rValMetAspValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThrAla 482
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         CGTGATGGATGTCGTCGAATATTTTACTGAGGCTGGATTCCCGGAGCAGGCGACAGCT   540

eGlnGluGlnGluIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspValLeu 502
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rGlyLeuSerIleArgLeuGlyProAlaLeuGlyIleTyrGluHisHisIleLysVal 522
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         CGGCCCTGTCCATCCGCCTCGGCCAGCCCTGAAAATCTACGACGACA-CACATCAAGGTG   659

uGlnGlnGlyHisGluPheGluAspProAspGlyPheLeuGly 538
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         TCAGCAAGGCCACTT-GAGGATGATGACCCCGATGGCTTCTTAGGC   706

1267   774 bp   mRNA   linear   EST 20-OCT-2000
32095F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917399 5',
sequence.
1267   GI:10350429
1267.1

sapiens (human)
sapiens
ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
bases 1 to 774)
MGC http://mgc.nci.nih.gov/.
onal Institutes of Health, Mammalian Gene Collection (MGC)
blished (1999)
act: Robert Strausberg, Ph.D.
1: cgapbs-r@mail.nih.gov
ue Procurement: ATCC/DCTD/DTP
A Library Preparation: Life Technologies, Inc.
A Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
. Sequencing by: Incyte Genomics, Inc.
ne distribution: MGC clone distribution information can be
d through the I.M.A.G.E. Consortium/LLNL at:
://image.llnl.gov
e: LLAM9743 row: n column: 24

Db 182 ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy 390 AspGluGlyArgGlyProAlaProGlySerGlyThrArgGlnValPheSerMetA
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 GATGAAGGACGGGGACCAGCCCGGGACGAGGCGCACCGCAGGTGTTCTCCATGC

Qy 410 MetAsnLysGluGlyGlyThrAlaSerValAlaThrGlyLeuProAspSerProSerI
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 ATGAACAAGGAGGGGGAACAGCTTCTTGTTGCCACCGGGCCAGACTCCCGTCC

Qy 430 ProLeuProProGlyLysProAlaLeuProGlyLysAlaAspGlyThrProPheGly
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Db 361 CCTTTGCCCCCAGGCAAACCAGCCCTACCTGGGCCAGACGGGACCCCCTTTGGC

Qy 450 ProGlyArgGlyLysGluLysProSerArgSerAspArgValGluTrpThrValMetAspVal
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Db 421 CCCGGGCGCAAAGAAGAGCCATCTGATCCCGTCGAGTGGACCGTGATGGATGTCC

Qy 470 TyrPheThrGluAlaGlyPheProGluGlnAlaThrAlaPheGlnGlnGluGlnGlu
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 TATTTTACTGAGGCTGGATTCCCGGAGCAGGCGACAGCTTTCCAAGAGCAGGAAA

Qy 490 GlyLysGlySerLeuLeuLeuMetGlnArgThrAspValLeuThrGlyLeuSerIle
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 GGCAAATCTTTGCTGCTCATGCAGCGCACAGATGTGCTCACCGGCTGTC--ATC

Qy 510 GlyProAlaLeuLysIleTyrGluHisHisIleLysValLeuGlnGlnGlyHis
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 599 GGGCCAGCCCTGAAAATCTACGAGCACCACATCAAGGTGCTTCAGCAAGGCCAC

Qy 530 AspAspAspProAspGly 535
         ||||||||||||||||||
Db 659 GATGATGACCCCGATGGT 676

RESULT 13
BM554748
LOCUS   BM554748   1057 bp   mRNA   linear   EST
DEFINITION AGENCOURT 6545443 NIH_MGC_88 Homo sapiens cDNA clone IMA(
            5', mRNA sequence.
ACCESSION   BM554748
VERSION   BM554748.1 GI:18794615
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute:
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom(
REFERENCE   1 (bases 1 to 1057)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNI
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information (
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12746 row: f column: 07
            High quality sequence stop: 557.
FEATURES   Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5736966"
                     /tissue_type="duodenal adenocarcinoma, cell lin(
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_88"
                     /note="Organ: small intestine; Vector: pCMV-SPO!
                     Site_1: NotI; Site_2: SalI; Cloned unidirection:

yHisPheGluAspAspAspProAspGlyPheLeu 537
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-CCACTTGAGGATTGATGACCCCGATGGGTTCTTA 754

424
4543F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677194 5',
sequence.
424
424.1   GI:9805144
sapiens (human)
sapiens
yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
lia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ases 1 to 858)
GC http://mgc.nci.nih.gov/.
nal Institutes of Health, Mammalian Gene Collection (MGC)
lished (1999)
ct: Robert Strausberg, Ph.D.
: cgapbs-r@mail.nih.gov
e Procurement: Louis M. Staudt, M.D., Ph.D.
Library Preparation: Ling Hong/Rubin Laboratory
Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Sequencing by: Incyte Genomics, Inc.
e distribution: MGC clone distribution information can be
through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
: LLCM352 row: f column: 11
quality sequence stop: 709.
Location/Qualifiers
1..858
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3677194"
/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_8"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

Length: 858
Matches: 1154.50
Conservative: 0
Mismatches: 3
Indels: 2
Gaps: 0

y: 98.67%
urity: 98.67%
         40.51%
         10

(1-538) x BE561424 (1-858)

SerAlaArgProSerArgSerLysArgGlyGlyGluGluValLeuGluLysGlu 329
|||||||||||||||||||||||||||||||||||||||||||||
AGCGCCCGCCCGTCTCGCGACCAAGAGAGGTGGAGAAGAGCGAGTACTTGAGAAAGAA 61

GluGluAspAspAspGlyGluAspGluGluAspGluGluAspAspAspValSerGluGlu 349
|||||||||||||||||||||||||||||||||||||||||||||
GAAGAAGATGATGATGAAGATGAAGATGAGGAAGATGATGTGTCAGAGGGCTCTGAA 121

ProGluSerAspArgProAlaGlyAlaValAlaGlnHisHisGlnLeuAsnGlyGluArgGly 369
|||||||||||||||||||||||||||||||||||||||||||||
CCCGAGAGTGACCGTCCTGCAGGTGCCCACCACAGCTTAACGGCGAGCGGGGA 181

GlnSerAlaLysValLysArgValLysGluThrProCysGlyGlyProHisGlnGlnGln 389

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LOCUS         BG116718                906 bp    mRNA      linear  EST
DEFINITION    6023174440F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:44
              mRNA sequence.
ACCESSION     BG116718
VERSION       BG116718.1  GI:12610224
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
  ORGANISM    Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hc
              1 (bases 1 to 906)
REFERENCE     NIH-MGC http://mgc.nci.nih.gov/,
AUTHORS       National Institutes of Health, Mammalian Gene Collectic
TITLE         Unpublished (1999)
JOURNAL       Contact: Robert Strausberg, Ph.D.
COMMENT       Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: ATCC
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LI
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution informatior
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAMI0150  row: p  column: 09
              High quality sequence stop: 693.
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4417784"
                     /tissue_type="duodenal adenocarcinoma, cell 1
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_88"
                     /note="Organ: small intestine; Vector: pCMV-S
                     Site_1: NotI; Site_2: SalI; Cloned unidirecti
                     oligo-dT primed. Average insert size 1.767 kb
                     enriched for full-length clones and construct
                     Technologies. Note: this is a NIH_MGC Library

ORIGIN

Alignment Scores:
Pred. No.:                                 Length:            906
Score:            3.29e-23                 Matches:           230
Percent Similarity:    1103.50             Conservative:        1
Best Local Similarity: 90.23%              Mismatches:         13
Query Match:           89.84%              Indels:             14
DB:                    38.72%              Gaps:                2
                       12

US-09-976-740-43 (1-538) x BG116718 (1-906)

Qy   266 GlyArgLeuThrArgGlyArgValGlnGlyLeuLeuGluGluGluAlaAlal
         |||||||||||||||||||||||||||||||||
Db    12 GGTCCACCCACGCGT----------------------CGGGCGGGCG

Qy   286 ArgLeuGluArgThrArgGlyAlaLeuAlaLeuAlaLeuProArgGlyAspArgl
         |||||||||||||||||||||||||||||||||||||||
Db    45 CGTCTGGACGCGCACCCGTCTCGGAGCGGCTTGCGCTGCCCGCGGGGGGACAGG!

Qy   306 AlaProProAlaAlaSerAlaAlaArgProSerArgSerLysArgGlyGlyGlut
         |||||||||||||||||||||||||||||||||||||||||||||
Db   105 GCGCCGCCGCCGCCGCCAGCGCCCGTCTCGCAGCAAGCAGGAGGTGGAGAI

Qy   326 LeuGluLysGluGluGluGluAspAspAspAspGluAspProGluGluAspGluAsp.
         |||||||||||||||||||||||||||||||:::||||
Db   165 CTTGGAGAAAGAAGAGGAAGAAGATGATGAAGATGATGAAGATGATGAAGAT

Qy   346 GluGlySerGluValPro-GluSerAspArgProArgProAlaGlyAlaGlnHisHi
         |||||||||||||||||: ||||||||||||||||||
Db   225 GAGGGCTCGAAGTGCCACGAGAGTGACCGTGCCCAGGTGGTGCCCAGCACCA

Qy   365 nGlyGluArgGlyProGlnSerAlaLysArgGlnValArgValGluTrpThrPr
         |||||||||||||||||||||||||||
```

3 (1-538) x BM554748 (1-1057)

```
B:                1.3e-23          Length:          1057
ity:              1119.50          Matches:          241
larity:           91.24%           Conservative:       9
                  87.96%           Mismatches:         9
                  39.28%           Indels:            15
                  12               Gaps:               3
```

```
lyLeuLeuGluGluGluAlaAlaAlaAlaArgGlyArgLeuArgThrArgLeuGlyAla    294
|||||||||||||||||||||||||||||||||||||||||||||||
GGCTGCTGGAGGAGGAGGAGGCGGCTCGAGGCCGTCCGAGCGCCACCCGTCTCGGAGCG   62

euAlaLeuProArgGlyAspArgProGlyArgProAlaProAlaAlaSerAlaArgPro    314
||||||||||||||||||||||||||||||||||||||||||||||
TTGCGCTGCCCCGCGGGACAGGCCCGACAGGCGCCGCCGCCGCCAGCGCCCGCCCCG    122

erArgSerLysArgGlyGlyGlyGluGluLeuGluLysGluGluGluGluAspAspAsp    334
||||||||||||||||||||||||||||||||||||||||||||||
CTCGCAGCAAGAGAGGGTGGAGAAGAGCCAGTACTTGAGAAAGAAGAAGAAGAGAGATGAT   182

aspGluAspGluAspGluAspAspAspValSerGluGluGlyLySerGluValProGluSerGluAsp    354
||||||||||||:::||||||||||||||||||||||||||
ATGAAGATGAAGATGATGATGAAGATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGAC   242

rgProAlaGlyAlaGlnHisHisGlnLeuAsnGlyLysGluArgGlyProGlnSerAlaLys    374
||||||||||||||||||||||||||||||||||||||||||
GTCCTGCAGGTGCCCAGCACCACCAGCTTAACGGCGAGCGGGACCTCAGAGTGCCAAG   302

GluArgValLysGluTrpThrProCysGlyGlyTrpProHisGlnGlnAspGluGlyArgGly    394
|||||||||||||||||||||||||||||||||||||
GAGAGGGTCAAGAGTGGACCCCCTGCGGACCCCAGAGCCACCAGGATGAAGGGCGGGGGG   362

ProAlaProGlySerGlyThrArgGlyGlnValPheSerMetAlaAlaMetAsnLysGluGly    414
|||||||||||||||||||||||||||||||||||||||
CCAGCCCCGGGCAGCCGGCCACCCGCCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGG   422

GlyThrAlaSerValAlaThrGlyProAspSerProSerProValProLeuProProGly    434
|||||||||||||||||||||||:::|||||||||||||
GGAACAGCTTCTGTTGCCACCGGGCCAGACTCCCCGTCCCCGTGCCTTGCCCCCAGGC   482

LysProAlaLeuProGlyAla-AspGly---ThrProPheGlyCysProProGlyArgGly    453
|||||||||||||||||||||| |||||||||||||
AAACCAGCCCTACCTGGGGCCCGACGGGGACCCCCCCTTTGGCTGTCCTCCCGGGGCCAA   542

sGluLys-ProSerAspProValGluThrGlyProThrArgValMetAspValValGluTyr--PheThr    472
||||||| |||||||||||||||||||:||||
AGAGAAGCCCATCTGATCCCGTCGAGTGACCGTGATGGATGTCGTCGAATATTTTTACT   602

GluAlaGlyPheProGluGluGlnAlaThrAla-PheGlnGln-GluIleAspGlyTyrLys    492
||||||||||||||||||||||| ||||||| :
GAGGCTGGATTCCCGGAGCAGGCGACAGCTTTTCAAGACAGGGAAATTGATCGCAAAA   662

er---LeuLeuLeuMetGlnArgThrAsp-ValLeu---ThrGlyLeuSerIle-ArgLeu    509
:: |||||||||||||||||:::|| ||
CCTTTGGTCTCATGCAGCCGCACAGATGGTGGCTCACCCGGCCGTGTCCCTTCCGCCTC   722

GlyProAla---LeuLysIleTyrGluHisHisIleLys--ValLeuGlnGlnGlyHisP    528
||||||       :: ||||||||:||:||
GGGGGCCAGCCCCTGCAAAAATCTACAAGCACCCCCTTCAGGGGGCCTTCCGCAAGGGCCACT    782

heGlu-AspAspAspPro  533
||||||| |||||||
TTGAAGGATGATGACCCC   800
```

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GGCGAGCGGGGACCTCAGAGTGCCAAGGAGAGGGTCAAGGAGGTGGACCCCCTGCGGACC 344

HisGlnGlyGlnGlyGluGlyArgGlyArgGlyProAlaProGlySerGlyThrArgGlnValPh 405
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CACCAGGGCCAGGATGAAGGGCGGGGGCCAGCCCCGGCAGCGGCCACCCGCCAGGTGTT 404

SerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThrGlyProAspSe 425
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TCCATGGCAGCCATGAACAAGGAAGGGGGAACAGCTTCTGTTGCCACCGGCCAGACTC 464

ProSerProValProLeuProProGlyLysProAlaLeuProGlyAlaAspGlyThrPr 445
|||||||||||||||||||||||||||||||||||||||||| |||||||||||  ||
CCGTCCCCGTGCCTTTGCCCCAGGCAAACCAGCCCTACCTGGGGCCGACGGGAC--CC 523

PheGlyCysProProGlyArgLysGluLysProSerProValGluTrpThrValMe 465
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TTTGGCTGTCCTCCCCGGCGCAAAGAAGAGAAGCCATCTGATCCCGTGGACCGTGAT 583

AspValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThrAlaPheGlnGl 485
|||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
GATGTCGTCGAATATTTTACTGAGGCTG--ATTCCGGAGCAGGCACAGCTTTCCAAGA 641

GlnGluIle--AspGlyLysSerLeu-LeuLeuMetGlnArgThrAspValLeuThrG 504
||||| ||||||||||||||||||||||||||||||||||||||||||||||||
CAGGAAATTTGATTGGGCAAATCTTTGCTGTCAATGAGCGCACAGATGTGCTCACCG 701

yLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis 518
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CCTGTTCATCCGTCCTTCGGCCAGCCTCGAAAATTTCGAGCCCAC 745
```

```
13784                686 bp    mRNA      linear    EST 07-AUG-2000
315608F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634417 5',
A sequence.
13784
13784.1    GI:9720996
o sapiens (human)
o sapiens
aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
malia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 686)
-MGC http://mgc.nci.nih.gov/.
ional Institutes of Health, Mammalian Gene Collection (MGC)
ublished (1999)
tact: Robert Strausberg, Ph.D.
il: cgapbs-r@mail.nih.gov
sue Procurement: Louis M. Staudt, M.D., Ph.D.
NA Library Preparation: Ling Hong/Rubin Laboratory
NA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
A Sequencing by: Incyte Genomics, Inc.
one distribution: MGC clone distribution information can be
nd through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
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        /clone_lib="NIH_MGC_8"
        /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
        EcoRI; cDNA made by oligo-dT priming. Directionally
        cloned into EcoRI/XhoI sites using the following 5'
        adaptor: GGCACGAG(G). Size-selected >500bp for average
        insert size 1.8kb. Library constructed by Ling Hong in
        the laboratory of Gerald M. Rubin (University of
        California, Berkeley) using ZAP-cDNA synthesis kit
        (Stratagene) and Superscript II RT (Life Technologies)."
```

ORIGIN

Alignment Scores:
Pred. No.:   1.23e-22   Length: 686
Score: 1080.00   Matches: 222
Percent Similarity: 96.52%   Conservative: 0
Best Local Similarity: 96.52%   Mismatches: 6
Query Match: 37.89%   Indels: 6
DB: Gaps: 0

US-09-976-740-43 (1-538) x BE513784 (1-686)

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Qy   310  AlaSerAlaArgProSerArgSerLysArgGlyGlyGlu-GluArgValLeuc
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Db     2  GCCAGCGCCCGCCCGTCTCGCACAAGAGAGGTGGAGAACGAGGCGAGTACTTG

Qy   329  luGluGluGluAspAspAspProAlaLeuProGlyAlaAspAspValSerGlu
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    62  AAGAGGAAGAAGATGATGATGACCAGCCCTGGGCCGACGGGAGATGATGTGTCAGAC

Qy   349  luValProGluSerAspArgProAlaGlyAlaGlnHisHisGlnLeuAsnGly
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   122  AAGTGCCCGAGAGTGACCGTCCTGCAGGTGCCCAGCCACCAGCTTAACGGC

Qy   369  lyProGlnSerAlaLysGluArgValLysGluTrpThrProCysGlyProHis
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Db   182  GACCTCAGAGTGCCAAGGAGGAGGGTCAAGGAGTGGACCCCCTGCGACCCGCAC

Qy   389  lnAspGlyLysArgGlyProAlaProGlySerGlyThrArgArgGlnValPheSer
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Db   242  AGGATGAAGGGCGGGGGCCAGCCCCGGCAGCGGCCACCCGCCAGGTGTTCTCC

Qy   409  laMetAsnLysGluGlyGlyThrAlaSerValAlaThrGlyProAspSerPro
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Db   302  CCATGAACAAGGAAGGGGGAACAGCTTCTGTTGCCACCGGGCCAGACTCCCCG

Qy   429  alProLeuProProGlyLysProAlaLeuProGlyAlaAspGlyThrProPhe
          |||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   362  TGCCTTGCCCCAGGCAAACCAGCCCTACCTGGGGCCGACGGGACCCCCTTT

Qy   449  roProGlyArgLysGluLysProSerProValGluTrpThrValMetAsp
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   422  CTCCCGGGCCAAAGAAGAGAAGCCATCTGATCCCGTGAGTGGACCGTGATGGAT

Qy   469  luTyrPheThrGluAlaGlyPheProGluGlnAlaThrAlaPheGlnGluGlr
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   482  AATATTTTACTGAGGCTGGATTCCCGGAGCAGGCAGCAGCTTTCCAAGAGCAC

Qy   489  spGlyLysSerLeuLeuLeuMetGlnArgThrAspValLeuThrGlyLeuSer
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Db   542  ATGGCAAATCTTTGCTGTCATGCAGCGCACAGATGTGCTCACCGGCCTGTCC

Qy   509  euGlyProAlaLeuLysIleTyrGluHisHisIleLysValLeuGlnGlnGly
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   602  TCGGGCCAGCCCTGAAATC-TACGAGCC-CACATCAAGGTGCTCAGCCAGC--

Qy   529  luAspAspProAlaGlyProPheLeu 537
          |||||||||||||||||| ||||
Db   658  AGGGTGATTG-CCCGATGGCTTCTTA 682
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Search completed: March 13, 2004, 04:01:57
Job time : 8144.53 secs

us-09-976-740-43.rge

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leic search, using frame_plus_p2n model

March 12, 2004, 19:49:56 ; Search time 8171.41 Seconds
(without alignments)
2853.675 Million cell updates/sec

US-09-976-740-43
2850
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BLOSUM62
Xgapop 10.0 , Xgapext   0.5
Ygapop 10.0 , Ygapext   0.5
Fgapop 6.0 , Fgapext   7.0
Delop   6.0 , Delext   7.0

3470272 seqs, 21671516995 residues

hits satisfying chosen parameters: 6940544

ength: 0
ength: 2000000000

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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RT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have
score greater than or equal to the score of the result being [
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Descript:
1	2850	100.0	1614	6	AR409337	AR409337
2	2850	100.0	1614	6	AX239602	AX239602
3	2850	100.0	1617	9	AY453840	AY453840
4	2616.5	91.8	12425	6	AR409341	AR409341
5	2616.5	91.8	12425	6	AX239607	AX239607
6	2594	91.0	2560	4	AY453841	AY453841
7	2594	91.0	2561	6	AR409339	AR409339
8	2594	91.0	2561	6	AX239605	AX239605
9	1983.5	69.6	237931	9	AC022098	AC022098
10	1560	54.7	1470	9	BC030129	BC030129
11	1455.5	51.1	1617	6	AR199530	AR199530
12	1455.5	51.1	1617	6	AR374682	AR374682
13	1455.5	51.1	1617	6	AR409317	AR409317
14	1455.5	51.1	1617	6	AX239568	AX239568
15	1455.5	51.1	1617	6	BD056444	BD056444
16	1269	44.5	982	7	BC007384	BC007384
17	1256.5	44.1	140795	2	AC079562	AC079562
18	1224.5	43.0	279020	2	AC133803	AC133803
19	1191.5	41.8	1422	6	AR199532	AR199532
20	1191.5	41.8	1422	6	AR374684	AR374684
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ALIGNMENTS

RESULT 1

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ice 45 from patent US 6632923.
337
337.1   GI:40160125

wn.
wn.
ssified.
ases 1 to 1614)
A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
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osing and treating atherosclerosis
: US 6632923-A 45 14-OCT-2003;
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          100.00%         Conservative:     0
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      HisGlyProGluGluArgThrArgAlaGluLeuGluLeuLysLeuGlnLeuGlnAsnArg   80
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      CACGGGCCCGGAGCCGGACCGCGCCGAGCTCGAGAAAACTGATCCAGCAGCGC     240

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      ProArgArgGlyAlaThrProProAlaProProAlaProArgGlyProAlaProAla  120
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      AlaAlaAlaAlaProAlaProProThrProAlaProProAlaProProAlaProVal  140
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      AlaAlaAlaProAlaArgAlaProAlaAlaAlaAlaAlaAlaAlaThrAlaProProPro  160
      ||||||||||||||||||||||||||||||||||||||||
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      ||||||||||||||||||||||||||||||||||||||||
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      |||||||||||||||||||||||||||||||||||||||
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Db  661  CCACAGCAGCAGCAGCCGCCGCCGCCGCAGCCACAGCCGCCGCCGCCGGAGGGGGGCCG

Qy  241  ArgAlaGlyAlaAlaAlaArgProValSerLeuArgGluValValArgTyrLeuG
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Db  721  CGGGCCGGCGGCGGCGGCGGCGGCCGGTGAGCCTGGGGAGGTGCGTGCGTACCTCG

Qy  261  SerGlyGlyAlaGlyGlyArgLeuThrArgGlyArgValGlnGlyLeuLeuGluG
         |||||||||||||||||||||||||||||||||||||||||||
Db  781  AGCGGCGGCGGCGGCGGGTCGCTAACCCGGGAGCCGCGGCTGCAGGGGCTGCTGGAGG

Qy  281  AlaAlaAlaArgGlyLeuGluArgThrArgLeuGlyAlaLeuAlaLeuProA
         |||||||||||||||||||||||||||||||||||||||
Db  841  GCGGCGGCGGCTCGAGGCCGTCTGAGGCGCACCCGTCTGGAGGCGCTTGCGCTGCCCC

Qy  301  AspArgProGlyArgGlyAlaProAlaAlaSerAlaAlaArgProSerArgSerLysA
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Db  901  GACAGGCCCGGACGGGGCGCCGCCGGCCGCCGCGCCCCGTCTCGCAGCAAGA

Qy  321  GlyGluGluArgValLeuGluLysGluGluGluGluAspAlaAspGluAspGluA
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Db  961  GGAGAAGAGCGAGTACTTGAGAAGAAGAGAAGAAGATGATGATGAAGATGAAG

Qy  341  GluAspAspValSerGluGlySerGluValProGluSerArgAspArgProAlaGlyA
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Db 1021  GAAGATGATGTGTCAGAGGGCTCTGAGTGCCCGAGAGTGACCGTCCTGCAGGTG

Qy  361  HisHisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluGluArgValLysG
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Qy  381  ThrProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProGlyS
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Qy  401  ThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyThrAlaSerV
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Qy  441  AlaAspGlyThrProPheGlyCysProProGlyArgGlyLysGluLysProSerAspF
         |||||||||||||||||||||||||||||||||||||
Db 1321  GCCGACGGGACCCCCTTTGGCTGTCCGCCCGGGCGCAAAGAGAAGCCATCTGATC

Qy  461  GluTrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGluC
         ||||||||||||||||||||||||||||||||||||
Db 1381  GAGTGGACCGTGATGGATGTCGTCGAATATTTTACTGAGGCTGGATTCCCGGAGC

Qy  481  ThrAlaPheGlnGluGlyIleAspGlyValSerLeuLeuLeuMetGlnArgT
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Db 1441  ACAGCTTTCAAGAGCAGGAGAAATTCATGATGGCAAATCTTTGCTGCTCATGCAGCA

Qy  501  ValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuIleTyrGluHisF
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RESULT 2
AX239602

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ACCESSION   AX239602
VERSION     AX239602.1  GI:15797275
KEYWORDS
SOURCE      Homo sapiens (human)
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,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
density liprotein binding proteins and their use in diagnosing
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arity:   100.00%       Mismatches:       0
                       Indels:           0
         6             Gaps:             0
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(1-538) x AX239602 (1-1614)

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Qy  181  ProProAlaProAlaAlaAlaProProAlaValAlaAlaProProAlaGlyProArgA
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Qy  241  ArgAlaAlaGlyGlyAlaAlaArgProValSerLeuArgGluValValArgTyrL
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Qy  281  AlaAlaAlaArgGlyArgLeuGluArgThrArgLeuGlyAlaLeuAlaLeuPr
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Qy  321  GlyGluGluArgValLeuGluLysGluGluGluAspAspAspAspGlu
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Qy  341  GluAspAspAlaSerGluGlySerGluValProArgSerAspArgProAlaGl
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Qy  361  HisHisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluArgValLys
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Qy  381  ThrProCysGlyProHisGlnGlyGlnAspGlyArgGlyProAlaProGl
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Qy  401  ThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyThrAlaSer
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840.1   GI:38565528

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sapiens
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ases 1 to 1617)
A.M., Deconinck,A.E., Campbell,B.D. and Lees,R.S.
in, a newly identified LDL-binding protein in human
osclerotic lesions
lished

ases 1 to 1617)
inck,A.E., Law,S.W., Lees,R.S. and Lees,A.M.
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3.26e-44   Length: 1617
2850.00   Matches: 538
y: 100.00%   Conservative: 0
rity: 100.00%   Mismatches: 0
                  Indels: 0
                  Gaps: 9

(1-538) x AY453840 (1-1617)

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Db   lLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIle  520
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Qy   181   ProProAlaProAlaAlaProProProAlaProAlaValAlaValAlaGlyProArgAr

Db   sValLeuGlnGlnGlyHisPheGluAspAspAspProAspProPheLeuGly  538
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3372  CCGCCCCGGCCAGCCGCTCCCCGGCGGTGGCGCCCCCGGCCCCCGCGCCGG
Qy   201   ProProAlaValAlaAlaArgGluProProProProGlnProProLeuProProGlnProPro

Db   GGTGCTTCAGCAAGGCCCACTTTGAGGATGATGACCCCCGATGGCTTCTTAGGC  1614
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3432  CCGGCCGCCGTCCCCGCCGGGAGCCCGCGTTGCCCGCCGCCCCGCCACAGCCGCC
Qy   221   ProGlnGlnGlnProProProProGlnProProGlnProProGluGlyGlyl

Db   3492  CCACAGCAGCAGCAGCCGCCGCCGCCCGCCGCAGCCGCCGCACAGCCGCCGCCGGCGGGGG
Qy   241   ArgAlaAlaGlyGlyAlaAlaAlaArgProValSerLeuArgGluValValArgTyrIle

Db   3552  CGGGGCCGGCCGGCGGCGGCGCGCCCGTGAGCCTGCGGGAAGTCGTGCGCTACCTC
Qy   261   SerGlyAlaGlyGlyAlaProGlyThrArgGlyArgValGlyGlnGlyLeuLeuGlyGlu

Db   3612  AGCGGCGGCGGCGCCCGGCGGTCGCCTAACCCGTGGCCCGCGTGCAGGGGGCTGCTGAC
Qy   281   AlaAlaAlaAlaArgGlyArgGluLeuGluArgThrArgGlyLeuGlyAlaLeuAlaLeuPro

Db   3672  GCGGGCCGGCTCGAGGCCGTCTCGGAGGCGCACCCCGTCTCGGAGCGCTTGCGCTGCGCCC
Qy   301   AspArgProGlyGlyAlaArgProGlyAlaProAlaAlaSerAlaArgProSerArg-----

Db   3732  GACACAGGCCCGAGACGGGCCCGGCGCCGCCCGCCGCCCGCCCGCCCCGTCTCGCAGCAAC
Qy   316   -----------------------------------------------------------

Db   3792  GCGGCCGGGGAGCGGGGGCGGCCGCCCGGGTGCGGGGCGGTGCGGGCGAAGTTGGTGGC
Qy   316   --------------------------------------------------------------

Db   3852  GCGAGTCCCCGGAGGAACTCGGTGCGCGGTGGCTTGCGGGCTTTGCGGCGCGTTTCC
Qy   316   --------------------------------------------------------------

Db   3912  CTTCGGTGCGTGGTGACCTTGCGAAGTGATTGAATCTCCCGGAGCCTCAGTTTCC
Qy   316   --------------------------------------------------------------

Db   3972  GTAAACGCGGTTTAATAACAGTAGCGACCCCCTTGGGGTTGTTGAGCGAGTTTAG
Qy   316   --------------------------------------------------------------

Db   4032  TTGGTTGTCGAGGGCTTTAGTTAACACAGAGCCTGGCACCGGAGTGAAATGCGTAA

Db   4092  GTCCGTATTGTTCTTAAAGGTGGAATCGGTTCCTCCTCCCCACCCGCCCCGGACGGC
Qy   317   -------------------------------------------------Ser
                                                              |||
```

ScaLeuArgValSerTyrLysGlySerIleSerTyrArgAsnAlaAlaArgValGln 100

9341   12425 bp   DNA   linear   PAT 18-DEC-2003
ence 50 from patent US 6632923.
9341
9341.1 GI:40160129

own.
.assified.
bases 1 to 12425
,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
density lipoprotein binding proteins and their use in
nosing and treating atherosclerosis
nt: US 663293-A 50 14-OCT-2003;
     Location/Qualifiers
     1. .12425
        /organism="unknown"
        /mol_type="genomic DNA"

:   Length: 12425
     1.69e-39   Matches: 536
     2616.50   Conservative: 0
ty: 69.16%   Mismatches: 2
arity: 69.16%   Indels: 239
     91.81%   Gaps: 4
     6

(1-538) x AR409341 (1-12425)

```
Qy   =AlaGlyProProAlaLeuProProProGluThrAlaAlaAlaAlaThrThrAlaAla  20
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3GCGGGGCCCCCGGCCCTACCCCGCCGGAGACGGCGGCGGCGGCCACCACCGGCGGCC  2891

Qy   aAlaSerSerAlaAlaSerProHisTyrGlnGluTrpIleLeuAspThrIleAsp  40
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   CGCCTCGCGTCGCCGCCGCTTCCCCGCCACTACCAAGACGTGGATCCTGGACACCATCGAC  2951

Qy   rLeuArgSerArgLysAlaArgGlyAlaArgProAspLeuGluArgIleCysArgMetValArgArg  60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3CTGCGCTCGCGCAAGGCGCGCGGCGCGCCGGACCTGGAGCGCATCTGCCGGATGGTGCGGCGG  3011

Qy   gHisGlyProGluProGluArgThrArgArgAlaGlyAlaLeuGluLysLeuGlnLysGlnGlnArg  80
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3CACGGCCCGGAGCCCGAGCGCACGCGCCGCGCCGGCGCCCTCGAGAAACTGCAGAAGCAGCAGC  3071
Qy   317                                                        -----Ser
                                                                     |||
```

```
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
REFERENCE   1
AUTHORS     Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
TITLE       Low density liprotein binding proteins and their use in d
            and treating atherosclerosis
JOURNAL     Patent: WO 0164874-A 50 07-SEP-2001;
            Boston Heart Foundation, Inc. (US)
FEATURES    Location/Qualifiers
source      1..12425
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:            1.69e-39        Length:         12425
Score:               2616.50         Matches:          536
Percent Similarity:  69.16%          Conservative:       0
Best Local Similarity: 69.16%        Mismatches:         2
Query Match:         91.81%          Indels:           239
DB:                  6               Gaps:               4

US-09-976-740-43 (1-538) x AX239607 (1-12425)
```

```
Qy    1  MetAlaGlyLeuProProGluProProGluThrAlaAlaAlaAlaThrThrA
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2832  ATGGCGGGGCCCCCGGCCCCTACCCCCGGCCCGGAGACGGCGGCGGCCACGG

Qy   21  AlaAlaSerSerAlaAlaSerProHisTyrGlnGluTrpIleLeuAspThrI
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2892  GCGGCCTCGTCGTCCGCGCTTCCCCGACTACCAAGAGTGGATCCTGGACACCA

Qy   41  SerLeuArgSerArgLysAlaArgProAspLeuGluArgIleCysArgMetValA
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2952  TCGCTGCGCTCGCGCAAGGCGCGGCCCGACCTGGAGCGCATCTGCCGGATGGTGC

Qy   61  ArgHisGlyProGluProGluArgThrArgAlaGluLeuGluLysLeuIleGlnG
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3012  CGGCACGGCCCGGAGCCGGAGCGCACGCGCGCCGAGCTCGAGAAACTGATCCAGC

Qy   81  AlaValLeuArgValSerTyrLysGlySerIleSerTyrArgAsnAlaAlaArgV
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3072  GCCGTGCTCCGGGTCAGCTACAAGGGAGCATCTCGTACCGCAACGCGGCGCGCG

Qy  101  ProProArgArgGlyAlaThrProProAspProArgAlaProArgGlyAlaP
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3132  CCGCCCCGCGGCGGACCGCCCCGGCCCGCGGGCGCCCCCGCGGGGCCC

Qy  121  AlaAlaAlaAlaAlaProProThrProAlaProProProProProProAlaP
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3192  GCGGCCGCCGCCGCCGCGGCCCGCCACCGCCCCGCCCCACCGCCCCGCCC

Qy  141  AlaAlaAlaAlaAlaProProAlaAlaArgAlaProAlaAlaAlaAlaThrAlaP
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3252  GCGGCCGCCGCCGCCGCCGGCGCCCGCGGCGGACGCGCGCCGCCGCCAGCGGC

Qy  161  SerProGlyProAlaGlnProGlyProArgAlaGlnAlaAlaProLeuAlaA
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3312  TCGCCTGGCCCGGGCCCCGCCGCGGGGCCGGGCGCCGGGCCCGGCGCCCTGGCCG

Qy  181  ProProAlaProAlaAlaProProAlaValAlaProAlaGlyProArgArgA
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3372  CCGCCCCGGCCGCCGCCGCTCCCCCGGGCGTGGCCGCCGCGGCCGGGCCGCGCGG

Qy  201  ProProAlaValAlaAlaAlaArgGluProProLeuProProProGlnProProA
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3432  CCGCCCCGGCCGTGGCCGCCGCCCGGGAGCCGCCGCTGCCGCCGCCGCAGCCGCCG

Qy  221  ProGlnGlnGlnGlnGlnProGlnProGlnProGlnProGluGluGlyGlyA
         |||||||||||||||||||||||||||||||||||||||||||||||||||
```

(column 2)

```
          GGTCTGGGATTAGAGACAGCTACTAATTTTGCATGCTTCTCTCCTCGGCTCCCAG-AGA  4210

Qy       GlyGluGlyArgValLeuGluLysGluGluGluGluGluAspAspAspGluGluAsp  339
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       GGAGAGAGCGAGTACTTGAGAAAGAGAAGAAGAAGAGATGATGATGAAGAT  4270

Qy       GluAspAspValSerGluGlyGluValProGluSerAspArgProAlaGlyGlyAla  359
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       GAAGATGATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCCTGCAGGTGCC  4330

Qy       HisHisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluArgValLysGlu  379
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       CACCACCAGCTTAACGGCGACGCGGGACCTTCAGAGTGCCAAGAGGAGGGTCAAGGAG  4390

Qy       ThrProCysGlyProHisGlnGlyGlnAsnGlyGluGluArgGlyArgGlyProGlySer  399
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       ACCCCCTGCGGACCCGACCGGACCAGGGCCACCAGGATGAAGGCGGGGGGCCAGCCCCGGCGAGC  4450

Qy       ThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThr----------  416
         |||||||||||||||||||||||||||||||||||||||||||||
Db       ACCCGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGAACAGGTAAGGAT  4510

Qy                                                              416
Db                                                              4570

Qy      429   --AlaSerValAlaThrGlyLeuProProSerProSerProProVal
              ||||||||||||||||||||||||||||||||||||||||||||
Db     4630   GGTGTTTTTCCTTCCCAGCTTCGTTGCCACCGGCCCAGACTCCCCGTCCCCGT

Qy      449   ProLeuProProGlyLysProAlaLeuProGlyTyrProProheGlyCysPr
              |||||||||||||||||||||||||||||||||||||||||||
Db     4690   TTTGCCCCCAGGCAAACCAGCCCACCTGGGGCCGACGGGACCCCCTTTGGCTGTCC

Qy      449
Db

Qy      457   AlaSerValAlaThrGlyLeuProProSerProSerProProArgGlyAspProArgAsp
              ||||||||||||||||||||||||||||||||||||||||||||||
Db     4750   AGTTGGGGTATTGGAGACATGGGGGTGCTGCTCAGGTGTGTCGGTACAGCCAGAGAGA

Qy            ------ProGlyArgLysGluLysProS
                    |||||||||||||||||||||||||
Db     4810   CCGTGTTCACTGGTGCTGTGTTTGTTTGATGCAGTCCCGGGCCAAAGAGAAGCCAT

Qy      477   ProProValGluTrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheP
              ||||||||||||||||||||||||||||||||||||||||||||
Db     4870   ATCCCCGTCGAGTGGACCGTGATGGATGTCGTCGAATATTTTACTGAGGCTGGATTCC

Qy      485   LeuGlnAlaThrAlaPheGlnGlu---------------------
              |||||||||||||||||||||||||||
Db     4929   AGCAGGCGACAGCTTTCCAAGA-GCAGGTGAGTTTCCAGCCCAGACTACACACTGA

Qy      485
Db     4989   ACACAGAGGGCCTCCCTGGGATGTGCCCTGGATCCCGGCTTTCTCTGTTCCTGTCCCA

Qy      505   GlnGluIleAspGlyLysLysSerLeuLeuLeuMetGlnArgThrAspValLeuThrGlyLyL
              |||||||||||||||||||||||||||||||||||||||||||||
Db     5049   AGGAAATTGATGGCAAATCTTTGCTGTCATGCAGCGCACAGATGTGCTCACCGGCC

Qy      525   erIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLysValLeuGlnGln
              |||||||||||||||||||||||||||||||||||||||||||||
Db     5109   CCATCCGCCTCGGGCCAGCCCTGAAAATCTACGAGCACCACCATCAAGGTGCTTCAGC

Qy      538   lyHisPheGluPheGluAspAspAspProAspGlyPheLeuGly
              |||||||||||||||||||||||||||||||||||||
Db     5150   GCCCACTTTGAGGATGATGACCCCGATGGCTTCTTAGGC
```

```
607          12425 bp    DNA        linear       PAT  26-SEP-2001
nce  50 from Patent WO0164874.
607
607.1   GI:15797282
```

```
Qy    429 1ProLeuProProGlyLysProAlaLeuProGlyAlaAspGlyThrProPheG:
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4631 GCCTTTGCCCCAGGCAAACCAGCCTACCTGGGGCCGACGGGACCCCCTTTG(

Qy    449 0---
Db   4691 GTAAGTTGGGTATTGGAGACATGGGGTGCTGCTCAGGTGTGTGGTACAGCC)

Qy    450 -------------------------------------------ProGlyArgLysGluE
Db   4751 CATCCGTGTTCACTGCGTGTCTGTTGTTTGATGCAGTCAGTCCCGGGCCAAAGAG)

Qy    457 erAspProValGluTrpThrValMetAspValValGluTyrPheThrGluAla(
              |||||||||||||||||||||||||||||||||||||||||
Db   4811 CTGATCCGTCGAGTGGACCGTGATGGATGTCGTGAATATTTTACTGAGGCTC

Qy    477 roGluGlnAlaThrAlaPheGlnGlu-------------------------
              |||||||||||||||||||||
Db   4871 CGGAGCAGGCGACCAGCTTTCCAAGA-GCAGGTGAGTTTCAGCCCAGGACTAC!

Qy    485 -----------------------------------------------------
Db   4930 CAGACACAGAGGGCTCCCTGGGATGTGCCCTGACTCCGGCTTTCTCTGTTCC1

Qy    486 --GlnGluIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspValLeu1
              ||||||||||||||||||||||||||||||||||||||||||||
Db   4990 CCCAGGAAATTGATGGCAAATCTTTGCTGCTCATGCAGCGCACAGATGTGCTCA

Qy    505 euSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLysValI
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5050 TGTCCATCCGCCTCGGGCCAGCCCTGAAAATCTACGAGCACCACATCAAGGTG(

Qy    525 lnGlyHisPheGluAspAspAspProAspGlyPheLeuGly 538
              ||||||||||||||||||||||||||||||||||||||||
Db   5110 AAGGGCCACTTTGAGGATGATGACCCCGATGGCTTCTTAGGC 5150
```

RESULT 6
AY453841

LOCUS   AY453841   2560 bp   mRNA   linear   MAM
DEFINITION   Oryctolagus cuniculus atherin mRNA, complete cds.
ACCESSION   AY453841
VERSION   AY453841.1 GI:38565530
KEYWORDS   .
SOURCE   Oryctolagus cuniculus (rabbit)
  ORGANISM   Oryctolagus cuniculus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
                Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE   1 (bases 1 to 2560)
  AUTHORS   Lees,A.M., Deconinck,A.E., Campbell,B.D. and Lees,R.S.
  TITLE   Atherin, a newly identified LDL-binding protein in human
                atherosclerotic lesions
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 2560)
  AUTHORS   Deconinck,A.E., Law,S.W., Lees,R.S. and Lees,A.M.
  TITLE   Direct Submission
  JOURNAL   Submitted (30-OCT-2003) Harvard-MIT Division of Health S
                Technology, Boston Heart Foundation, 139 Main Street, Ca
                02142, USA
FEATURES   Location/Qualifiers
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                     /isolation_source="healing ballooned aorta"
                     /db_xref="taxon:9986"
                     /tissue_type="aorta"
     CDS   246..1898
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                     /product="atherin"
                     /protein_id="AAR24088.1"
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                     /translation="MAGPPALPPPETAAAATTAAAAASSAASPHYQ

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Qy   3551 ACAGCAGCAGCGCCGCCGCCGCCGCCAGCCGCCGCCGGAGGGGCGCGGTG
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Db    260 gAlaGlyGlyAlaAlaArgProValSerLeuArgGluValValArgTyrLeuGlyGly
              |||||||||||||||||||||||||||||||||||||||||||||||||
       3611 GGCGGGGGGCGGCGGCGGCGGCCCGAGCCGTGCGGCGAAGTCGTGCGCTACCTCCGGGGGC

Qy    280 rGlyGlyAlaGlyGlyArgLeuThrArgGlyValArgValGlnGlyLeuLeuGlyGluGlu
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3671 CGGCGGCGGCCGGCGTCGCTAACCCGGGGCCCGTGCGAGGGGCGTGCTGGAGGAGGAG

Qy    300 aAlaAlaAlaArgGlyAlaArgGlyThrArgGlyLeuGlyAlaAlaLeuAlaLeuProArgGly
              |||||||||||||||||||||||||||||||||||||||
Db   3731 GGCGGGTCGAGGCGTCTGAGCGCACCCGTCTCGGAGGCGCCTGCGCTGCCCCCGCGGG

Qy    316 pArgProGlyArgAlaProProAlaAlaSerAlaArgProSerArg----------
              ||||||||
Db   3791 CAGGCCCCGGACGGGCGGCGCCCCGGCCGGCCCCGTCTCGCAGCAAGGTGAGC

Qy    316 -----------------------------------------------------
Db   3851 GCCGGGGAGCGGGGGCGCGCCGCGGGTGGGCAGTGGCGCGGGGCGAAGTTGGTGGCGGGGGC

Qy    316 -----------------------------------------------------
Db   3911 GAGTCCCGGGAGGAACTGGGTGCGGGTGGCGGTGGGCGTTTGCGCGGTTCCTGCGGG

Qy    316 -----------------------------------------------------
Db   3971 CGGTGCCTGCGTGGTCGACCTTGGCAAGTGTGATTGAATCTCCCGGAGCCTCAGTTCCTCCGCT

Qy    316 -----------------------------------------------------
Db   4031 AAACGCGGTTTAATAACAGTAGCGACCCCTTGGGGTTGTTGAGCGAGTTAGTAAGAT

Qy    316 -----------------------------------------------------
Db   4091 GGTTGTCGAGGGCTTTAGTTAACACAGAGCCTGGCACGGAGTGAATGCGTAAAAGTTA

Qy    316 -----------------------------------------------------
Db   4151 CCGTATTGTTCTTAAAGGTGAATCGGTTCCTCCTCCCCACCGCCCGGACGCCACAGT

Qy    319 -------------------------------------SerLysArg
                                                    |||
Db   4210 GGGTCTCGGATTAGAACAGCTACTAATTTGCATGCTTCTCTCCGCTCCAG-AGA

Qy    339 yGlyGluGluArgValLeuGlyValGluLysGluGluAspAspAspGluAspGluAsp
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4270 TGGAGAAGAGCCAGTACTTGAGAAGAGAAGAGGAGAAGAAGATGATGAAGATGAAGAT

Qy    359 jGluAspAspValSerGluGlyGlySerGluValProGluSerAspArgProAlaGlyAla
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4330 AGAAGATGATGTGTCAGAGGGCTCGAAGTGCCCGAGAGTGACCGTCCTGCAGGTGCC

Qy    379 zHisHisGlnLeuAsnGlyValArgGlyProGlnSerAlaLysArgValLysGlu
              ||||||||||||||||||||||||||||||||||||||
Db   4390 GCACCACCAGCTTAACGGCGAGCGGGGACCTCAGAGTGCCAAGGAGGGGTCAAGGAG

Qy    399 pThrProCysGlyProHisGlnGlyValGlnAspGlyLeuAspGlyLysArgGlyProAlaProGlySer
              ||||||||||||||||||||||||||||||||||||||
Db   4450 GACCCCCTGCCGACCCCGCACCCAGGGCCACGAGGATGAAGGGCGGGGACCCCGGGCAGC

Qy    416 yThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyThr----------
              ||||||||||||||||||||||
Db   4510 CACCCGCCAGTGTTCTCCATGGCAGCCATGAACAAGGAGGGGAACAGGTAAGGAT

Qy    416 -----------------------------------------------------
Db   4570 CTCTGGGTGGGAAGAGTGCTAGGTGAGAGAGAACTCAGCCCGAAGACAAAGCCAAAG

Qy    429 -------AlaSerValAlaThrGlyLeuProAspSerProSerProVa
                                         ||||||||||||||||||||
Db   4630 AGGTGTTTTTTCCTTCCCAGCTTCTGTTGCCACGGGGCCAGACTCCCCGTCCCCCGT
```

```
SRKARPDLERICRMVRRHGPEPERTRAELEKLIQQRAVLRVSYKGSISYRNAARVQP
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QRTDVLTGLSIRLGPALKIYEHHIKVLQQGHFEDDDPRGFLG"


       1.68e-39            Length:        2560
       2594.00             Matches:       503
y:     94.20%              Conservative:  17
rity:  91.12%              Mismatches:    16
       91.02%              Indels:        16
       4                   Gaps:          8


(1-538) x AY453841 (1-2560)


AlaGlyProProAlaLeuProProProGluThrAlaAlaAlaAlaThrThr---Ala      19
|||||||||||||||||||||||||||||||||||||||
GCGGGCCCCCCGCCCCTACCCCCGCGGACACGGGCGGCGGCCGCCACCGGCCGCG       305

AlaAlaSerSerSerAlaAlaSerProHisTyrGlnGluTrpIleLeuAspThrIle      39
|||||||||||||||||| :::|||||||  |||||||||||
GCCGCCTCGTCGTCGCCGCTTCCCCGCACTACCAAGAGTGGATTCTGGACACCATC      365

SerLeuArgSerArgLysAlaArgProAspLeuGluArgIleCysArgMetValArg      59
||||||||||||||||||||||||||||||||||||||||||||
TCGCTGCGCTCGCGCAAGGCCCGCGACCTGGAGCGCATCTGCCGGATGGTGCCG       425

ArgHisGlyProGluProGluThrArgAlaAlaGluLeuGluLysLeuIleGlnGln      79
||||||||||||||||||||||||||||||||||||||||||
CGGCACGGCCCCGAGCCGGAGACGCGGGCAGCTCGAGAAACTGATCCAGCAG       485

AlaValLeuArgValSerTyrLysGlySerIleSerTyrArgAsnAlaAlaArgVal      99
||||||||||||||||||||||||||||||||||||||||||
GCCGTGCTCCGGGTCAGCTACAAGGGAGCATCTCGTACCGCAACGCGGCGCGTC      545

ProProArgArgGlyAlaThrProProAlaProProArgGlyAlaProGlyAlaPro     119
|||||||||||||||||||||||||||||||||||||
CGCCCGCGGCGCGGAGCCACCCCGCCCGCCCCGCCGCGCGGGGCCCC      605

AlaAlaAlaAlaAlaAlaProProThrProAlaProProProProAlaPro         139
|||||||||||||||||||||||||||||||||||
-GCCGCCGCCGCCGCCGCCGCGCTCCCCCCGGCAGCGGCCCCGGCCGGCCCCG      659

--AlaAlaAlaAlaAlaArgAlaArgProArg-----AlaAlaAlaAlaAlaAla     156
||||||||||||||||||||||        ||||||||||||
GCCGCGGCGCGGGCGCCCGGGCGCCCCGGGGAGTCGCCGCTGCCGCCGCCGCC      719

AlaProProSerProGlyProAlaGlnProGlyGlnGln-----------ProProProPro     176
|||||||||||||||||||||||||            |||||||||||
CAGCCCGCCCGCCCGGGCCACAGCAGCAGCCAGCCGCCACGCCCGCCCGCCCAG      959

ProGlnProProProGlyGluValValArgValAlaValAlaArgGlyAlaAlaProVal     249
|||||||||||||||||||||||||||||||||||||||||
CCACAGCCGCCCGCCGAGGGGGCGCGCCGGCCCGGCGCCGGCGGCCCCGTG      1019
```

```
SerLeuArgGluValValArgTyrLeuGlyGlySerGlyGlyAlaGlyGlyArgL        250
|||||||||||||||||||||||||||||||||
AGCCTGCGGGAAGTCGTGCGCTACCTCGGGGGTAGCAGCGGCGCTGGCGGCCGCC       1020

ArgGlyArgValGlnGlyLeuLeuGluGluBAAAlaAlaAlaArgGlyArgLeuG        270
|||||||||||||||||||||||||||||||||||||
CGCGGCCGCGTCGCAGGGTCTGCTGGAAGAGGAGGCGGCGGCGGGCCGCCTGG      1080

ThrArgLeuGlyALaLeuALaLeuProArgGlyAspArgProGlyArgAlaProP       290
||||||||||||||||||||||||||||||||||||
ACCCGRCTCGGAGCGTTGCGCTGCCCCGCGCGGGACAGGCCCGGACGGGGCCCAC      1140

AlaSerAlaAlaArgProSerArgLysArgGlyGlyGluGluValLeuGluL        310
:::|||||||| :::|||||:::|||||||||
GCCAGCGCCGGCCGCCGCGAACAAGAGACTGGCGGAGGAGGAGTGCTTGAAA       1200

GluGluGlnAspAspAspAspValValAspGluGluAspAsp------ValSerG       330
|||||:::||  :::|||||::||||||
GAGGAGGAGGAGGAGGAAGCACGAGGACGACGACGACGTCGTGTCCG       1260

SerGluValProGluSerAspArgProAlaGlyAlaGlnHisHisGlnLeuAsn-       348
||||:::||||||||||||||||||||||||
TCGGAGGTGCCCGAGAGCGATCGTCCCGGGGTGCCGCAGCATCACCAGCTGAATG      1320

GluArgGlyProGlnSerGluArgGlyPheProGlnThrProCysGlyP       367
:::|||||||||||||||||||||||||||||||
GAGCGCGGCCCCAGACCGCCAAGGAGGTGGTCGCTGTGTGGCC          1380

GlnGlyGlnAspGluGluGlyArgGlyAlaProGlySerGlyThrArgGlnValP       387
|||||||||||||||||||||||||||||||||||||
CCTGGCCAGGAGGAAGGGCGGGAGCCGGCAGTGGCACCCGCCAGGTGT         1440

MetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThrGlyProAspS       407
||||:::||||||||||||||||||||||||
ATGGCGGCCTTGAGTAAGGAGGGGGGATCAGCCCTCTTCGACCACCGGCCCTGACT      1500

SerProValProLeuProProGlyLysProSerAspProValGluTrpThrP       427
|||||||||||||||||||||||||||||||||||
TCCCGGTGCCTTTGCCCCCGGAAGCCCGTCCCCAGGAGCCGATGGGACCC       1560

GlyCysProProGlyArgLysProSerAspProValGlnThrValM       447
||||||||||||||||||||||||||||||||
GGCTGCCCTGCCGGGCGCAAAGAGAGCCGGACAGACCCCGTGGAGTGGACAGTCA       1620

ValValGluTyrPheThrGluAlaGlyPheProGlnAlaThrAlaPheGlnG       467
||||||||||||||||||||||||||||||||
GTCGTGGAGTACTTCACCGAGGCCGGCTTCCCTGAGCAAGCCACGGCTTTCCAGG      1680

GluIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspValLeuThrGlyL       487
||||||||||||||||||||||||||||||||||
GAGATCGACGGCAAGTCCCTGCTCATCGAGACCGATGTCCTCACCGGCC       1740

IleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLysValLeuGlnG       507
||||||||||||||||||||||||||||||
ATCCGCCTGGGGCCCAGCGTGAAAATCATGAGCACCATATCAAGGTGCTGCAGC      1800

HisPheGluAspAspAspProGlyPheLeuGly       527
|||||:::|||||||||||||
CACTTCGAGGACGATGACCCCGGAAGGCTTCCTGGGA       1860
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RESULT 7
AR409339
LOCUS   AR409339   2561 bp   DNA   linear   PAT 1
DEFINITION   Sequence 48 from patent US 6632923.
ACCESSION   AR409339
VERSION   AR409339.1   GI:40160127
KEYWORDS
SOURCE   Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 2561)
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density lipoprotein binding proteins and their use in

nosing and treating atherosclerosis
nt: US 6632923-A 48 14-OCT-2003;
Location/Qualifiers
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ty:     94.20%                  Conservative:   17
arity:  91.12%                  Mismatches:     16
        91.02%                  Indels:         16
        6                       Gaps:           8
```

(1-538) x AR409339 (1-2561)

```
Qy    270 ArgGlyArgValGlnGlyLeuLeuGluGluGluAlaAlaAlaAArgGlyArgLei
              |||||||||||||||||||||||||||||||  ||||||||||/|/////|
Db   1080 CGCGGACCGCGTGCAGGGTCTGCAGGGTGCTGCTGGAAGAGGAGCCGGCGGGGCCGGGGCGCGC\
```

```
Qy    290 ThrArgLeuGlyAlaLeuAlaLeuProArgGlyArgProGlyArgAlaPr\
              ||||||||||||||||||||||||||||||||||||||||||||
Db   1140 ACCCGTCTCGGAGCGGCTTGCCGTCCCCGCCGGGGACAGGCCCGGACGCGGCGGCGC\
```

```
Qy    310 AlaSerAlaArgProSerArgSerLysArgGlyGlyGluGluArgValLeuGl\
              ||||||||||    :::|||||||||||
Db   1200 GCCAGCGCCCCGGCCCGGCCGGGCGCGGGCGGAAGAAGAAGAGGAGAGAGGAGCTTGA\
```

```
Qy    330 GluGluAspAspAspGluAspAspGluAspAspAsp------ValSer
              |||:::|||||||||||||||||||||||
Db   1260 GAGGAGGAGGAGGAGGAAGAAGACGACGAGGAGACGACGACGTCGTGTC\
```

```
Qy    348 SerGluValProGluSerAspArgProAlaGlyAlaGlnHisHisGlnLeuLeuAsi
              |||||||||||||||||||||| ::::||||||||||||
Db   1320 TCGGAGGTGCCCGAGAGCGAATCGTCCCGCGGGGTGCTGCAGCATCACCAGCTGAA\
```

```
Qy    367 GluArgGlyProGlnSerAlaLysArgValLysGluThrProCysGl\
              ||||||||||||| :::|||||||||||
Db   1380 GAGCGGCGGCCCCAGACCGCCAAGGAGCGGGGCCAAGGAGTGTCGCTGTGTGG(
```

```
Qy    387 GlnGlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThrArgGlnVal
              || ::::|||||||||||||||||
Db   1440 CCTGGCCAGGAGGAAGGGCGGGGCCCGGCCCGGGCAGTGGCCACCCGCCAGGTC
```

```
Qy    407 MetAlaAlaMetAsnLysGluGluProAlaGlyGlyThrAlaSerValAlaThrGlyTyrProAsp\
              ||||||| :::||||||||||||||||||
Db   1500 ATGGCGGCCCTGAGTAAGGAGGGGGGATCAGCCTCTTCGACACCGGGCCTGAC
```

```
Qy    427 SerProValProLeuProProGlyProGlyLysProAlaLeuProGlyAlaAspGlyThr\
              ||||||| :::|||||||||
Db   1560 TCCCCGGTGCCTTTGCCCCCGGAAGCCGGCCCTCCCAGGAGCCGATGGGACC
```

```
Qy    447 GlyCysProProGlyArgGluLysProSerAspProValGluTrpThrVal
              ||||||||||||||||||
Db   1620 GGCTGCCCTGCCGGGCGCAAAGAGAAGCCCGAGACCCCGTGGAGTGGACAGTC
```

```
Qy    467 ValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThrAlaPheGln
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Db   1680 GTCGTGGAGTACTTCACCGAGGCGGCTTCCCTGAGCAAGCCACCGGCTTTCCAC
```

```
Qy    487 GluIleAspGlyGlyLysSerLeuLeuLeuMetGlnArgThrAspValLeuThrGlyGly
              |||||||||||||||||||||||||||
Db   1740 GAGATCGACGGCAAGTCCCTGCTCATGCAGCGCACCGATGTCCTCACCGGC
```

```
Qy    507 IleArgLeuGlyProAlaLeuLysIleTyrGluHisHisGlyIleLysValLeuGln
              |||||||||||||||||
Db   1800 ATCCGCCTGGGGCCAGCGTTGAAAATCTATGAGCACCATATCAAGGTGCTGCAG
```

```
Qy    527 HisPheGluGluAspAspProAspGlyPheLeuGly 538
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Db   1860 CACTTCGAGGAGGACGATGACCCGGAAGGCTTCCTGGGA 1895
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RESULT 8
AX239605
LOCUS   AX239605   2561 bp   DNA   linear   PAT
DEFINITION   Sequence 48 from Patent WO0164874.
ACCESSION   AX239605
VERSION   AX239605.1   GI:15797279
KEYWORDS   .
SOURCE   Oryctolagus cuniculus (rabbit)
  ORGANISM   Oryctolagus cuniculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
             Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE   1
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density liprotein binding proteins and their use in (
             and treating atherosclerosis
  JOURNAL   Patent: WO 0164874-A 48 07-SEP-2001;

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```

```
aAlaAlaSerSerSerAlaAlaSerProHisTyrGlnGluTrpIleLeuAspThrIle 39
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CGCCGGCCTCGTCGTCCCGCCGCTTCCCCGCACTACCAAGAGTGGATTCTGGACACCATC 365
```

```
pSerLeuArgSerArgArgLysAlaArgProAspLeuGluArgIleCysArgMetValArg 59
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CTCGCTGCGCTCGCGGCAAGGCGCGGCGACCTGGAGCGCATCTGCCGGATGGTGCGG 425
```

```
gArgHisGlyProGluArgThrArgAlaGluLeuGluLeuGlnGln 79
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SCGGCACGGCCCCGGAGCGCGGAGCCACGCGCTCGAGAAACTGATCCAGCAG 485
```

```
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CGCCGTGCTCCCGGGTCAGCTACAAGGGAGCATCTCGTACCGCAACGCGGCGCGGTC 545
```

```
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    |||||||||||||||||||||||||||||||
CGCCGCCGGCGCGGAGCCCCGCCGCCGCCCCGCCGCCGCGCGCGGGGGGCCCC 605
```

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aAlaAlaAlaAlaAlaProProThrProAlaProProProAlaProProAlaProAlaPro 139
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```
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```

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Heart Foundation, Inc. (US)

Location/Qualifiers
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QRTDVLTGLSIRLGPALKIYEHHIKVLQQGHFEDDDPEGFLG"

1.68e-39   Length: 2561
2594.00   Matches: 503
94.20%   Conservative: 17
91.12%   Mismatches: 16
91.02%   Indels: 16
6   Gaps: 8

(1-538) x AX239605 (1-2561)

| Qy | 197 | ArgArgAlaProPro------AlaValAlaAlaAlaArgGluProProLeuProP |
| Db | 840 | CGCCGCGCCCCCCGGCGCCCCCGGCCCGTCGCCGCCCGGGAGTCGCCGCTGCCGCG |

| Qy | 215 | ProGlnProProAlaProProGlnGlnGln------------ProProP |
| Db | 900 | CCACAGCCGCCCGGCGCCGCCACAGCAGCAGCAGCCGCCGCGCCCGCC |

| Qy | 230 | GlnProGlnProProProGluProGlyAlaValAlaArgAlaGlyAlaAlaArgP |
| Db | 960 | CAGCCACAGCCGCCCGCCCGAGGGGGCGCCGCGGGGCGGCCCGGGCCGGGC |

| Qy | 250 | SerLeuArgGluValValArgTyrLeuGlyGlySerGlyGlyAlaGlyGlyArgL |
| Db | 1020 | AGCCTGCGGGAAGTCGTGCGCTACCTCGGGGGTAGCAGCGGCGGCGCCGGCCGCC |

| Qy | 270 | ArgGlyArgValGlnLeuLeuGluGluAlaAlaAlaArgGlyArgLeuG |
| Db | 1080 | CGCGGCGCCGTGCAGCTGCTGGAAGAAGGAGGCGGCGCGCGGGGGCGCCTGG |

| Qy | 290 | ThrArgLeuGlyAlaLeuAlaLeuProArgGlyAspArgProGlyArgAlaProP |
| Db | 1140 | ACCCGTCTCGGAGCGCTTGCGCTGCCCCCGGGGCGACAGGCCCGGACGCGGCGCCAC |

| Qy | 310 | AlaSerAlaArgProSerArgSerLysArgGlyGlyGluArgValLeuGluL |
| Db | 1200 | GCCAGCGCCCGCGGGGGGCGGAACAAGAGAGCTGGCGAGGAGCGAGTGCTTGAAA |

| Qy | 330 | GluGluGluAspAspAspGluAspAspAspAsp------ValSerG |
| Db | 1260 | GAGGAGGAGGAGGACGAGGACGACGACGACTCGTCCG |

| Qy | 348 | SerGluValProGluSerAspArgProAlaGlyAlaGlnHisHisGlnLeuAsn- |
| Db | 1320 | TCGGAGGTGCCCGAGAGCGATCGTCCCGCCGGTGCGCAGCATCACCAGCTGAATG |

| Qy | 367 | GluArgGlyProGlnSerAlaLysGluArgValLysGluTrpProThrProCysGlyP |
| Db | 1380 | GAGCGCGGCCGCCCAGACCGCCAAGGAGCGGGTCCGTGTGGCC |

| Qy | 387 | GlnGlyGlnAspProGluGlyArgGlyProAlaProGlySerGlyThrArgGlnValP |
| Db | 1440 | CCTGTGCCAGGAGGAAGGGGGGGCCGGGCAGTGGCACCCGCCCAGGTGT |

| Qy | 407 | MetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThrGlyProAspS |
| Db | 1500 | ATGGCGGCCTTGAGTAAGGAGGGGGGGATCAGCCTCTTGACCACCGGGCCTGACT |

| Qy | 427 | SerProValProLeuProProGlyLysProAlaLeuProGlyAlaAspGlyThrP |
| Db | 1560 | TCCCCGGTGCCTTTGCCCCCGGAAGCCAGCCCTTCCCAGGAGGCCGATGGGACCC |

| Qy | 447 | GlyCysProProGlyArgLysGluLysProSerAspProValGluTrpThrValM |
| Db | 1620 | GGCTGCCCTGCCCGGCCAAAGAAGAGCCCGAGACCCCGGAGTGGACAGTCA |

| Qy | 467 | ValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThrAlaPheGlnG |
| Db | 1680 | GTCGTTGGAGTACTTCACCGAGGCCGGCTTCCCTGAGCAAGCCACGGCTTTCCAGG |

| Qy | 487 | GluIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspValLeuThrGlyL |
| Db | 1740 | GAGATCGACGGCAAGTCCCTGCTCATGCAGCGCACCGATGTCCTCACCGGCC |

| Qy | 507 | IleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLysValLeuGlnG |
| Db | 1800 | ATCCGCGTGGGGCCAGCGTTGAAAATCATATGAGCACCATATCAAGTGCTGCAGC |

| Qy | 527 | HisPheGluAspAspAspProAspGlyPheLeuGly 538 |
| Db | 1860 | CACTTCGAGGACGATGACCCGGAAGGCTTCCTGGGA 1895 |

AlaGlyProProAlaLeuProProProGluThrAlaAlaAlaAlaThrThr---Ala 19
||||||||||||||||||||||||||||||||||||||| ||
CGGGGCCCCCCGGCCCTACCCCCCGGAGACGGCGGCG 305

AlaAlaSerSerAlaAlaSerProHisTyrGlnGluTrpIleLeuAspThrIle 39
|||||||||||||||||||||||||||||||||||||||||:::
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SerLeuArgSerArgLysAlaArgProAspLeuGluArgIleCysArgMetValArg 59
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ArgHisGlyProGluProGluArgThrArgAlaGluLeuGluLysLeuIleGlnGln 79
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ACGGCACGGGCCCGGAGCCGGAGCGCACCGCGGCTGAGAAACTGATCCAGCAG 485

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BCCGTGCTCCGGGTCAGCTACAAGGGGAGCATCTCGTACCGCAACGCGGCGGCGTC 545

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---AlaAlaAlaAlaAlaProAlaProAlaArg------AlaAlaAlaAlaAla 156
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AlaProProSerProGlyProAlaGlnProGlyProArgAlaGlnArgAlaAlaPro 176
|||||||||||||||||||
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arity:   55.48%           Mismatches:           2
         69.60%           Indels:             345
         9                Gaps:                 5

(1-538) x AC022098 (1-237931)
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Qy    101 ProProArgArgGlyAlaThrProProAlaProProArgAlaProArgGlyAl.

Db 127497 CCGCCCCGGCGGCGGAGCCACCCGCCGGCC------
          ||||||||||||||||||||||||||
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Db 127468 ------
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Db 127468 ------
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Db 127468 ------
Qy    181 ProProAlaProAlaAlaProAlaValAlaProProAlaGlyProArgArt

Db 127468 ------
Qy    201 ProProAlaValAlaAlaArgGluProProLeuProProProProGlnProPro

Db 127467 ----CCGCCC
          ||||||
Qy    221 ProGlnGlnGlnProProProGlnProProProProGluProGly

Db 127455 CCACAGCAGCAGCAGCCGCCGCCGCCGCCGCCGCCACAGCCGGGGGGG
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Qy    241 ArgAlaGlyGlyAlaAlaAlaArgProValSerLeuArgGluValValArgTyrLeu

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          |||||||||||||||||||||||||||||||||||
Qy    261 SerGlyGlyAlaGlyGlyArgArgGlyArgValGlnGlyLeuLeuGlu

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Qy    301 AspArgProGlyArgGlyArgAlaProProAlaAlaSerAlaArgProSerArg------

Db 127215 GACAGGCCCGGACAGGCGGCCCGGCCGCCCCAGCGCCCGCCGTCTCGCAGCAAG
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Qy    316 ------

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Qy    317 ------Ser.
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:AlaSerSerAlaSerAlaAlaSerProHisTyrGlnGluTrpIleLeuGluAspThrIleAsp 40
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:LeuArgSerArgLysValAlaArgProAspLeuGluArgIleCysArgMetValArg 60
 |||||||||||||||||||||
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:HisGlyProGluArgThrArgAlaGlyGluLeuLysLeuIleGlnGlnArg 80
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```

```
KEYWORDS        .
SOURCE          Homo sapiens (human)
  ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1  (bases 1 to 1470).
  AUTHORS       Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
                Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
                Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
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                Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
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                Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
                Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
                Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
                Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,
                Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
                Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE         Generation and initial analysis of more than 15,000 full-length
                human and mouse cDNA sequences
  JOURNAL       Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   MEDLINE      22388257
   PUBMED       12477932
REFERENCE       2  (bases 1 to 1470)
  AUTHORS       Strausberg,R.
  TITLE         Direct Submission
  JOURNAL       Submitted (07-MAY-2002) National Institutes of Health, Mammalian
                Gene Collection (MGC), Cancer Genomics Office, National Cancer
                Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                USA
  REMARK        NIH-MGC Project URL: http://mgc.nci.nih.gov
  COMMENT       On Aug 19,2003 this sequence version replaced gi:2253961
                Contact: MGC help desk
                Email: cgapbs-r@mail.nih.gov
                Tissue Procurement: DCTD/DTP
                cDNA Library Preparation: Rubin Laboratory
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: National Institutes of Health Intramural
                Sequencing Center (NISC),
                Gaithersburg, Maryland;
                Web site: http://www.nisc.nih.gov/
                Contact: nisc mgc@nhgri.nih.gov
                Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
                Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
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                Young,A., Zhang,L.-H. and Green,E.D.
                Clone distribution: MGC clone distribution information can be found
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In many cases mediates homodimerisation"
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(1-538) x BC030129 (1-1470)
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Qy    aGlyGlyArgGlyLeuThrArgGlyArgValGlnGlyLeuLeuGluGluGluAlaAlaAla    283
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Qy    gGlyArgLeuGluArgThrArgLeuGlyAlaLeuAlaLeuProArgGlyArgAspArgPro    303
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Qy    yArgAlaProAlaAlaSerAlaArgAlaArgProSerArgSerLysArgGlyGlyGluGlu    323
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Qy    yValLeuGluLysGlyGluGluGluArgGlyLeuAspProAspAspGluAspGluAspAsp    343
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Qy    lPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThrGlyPro     423
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Qy    AspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAlA        424
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Qy    ThrProPheGlyCysProProGlyArgLysGluLysProSerAspProValGly        444
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    ACCCCCTTTGGCTGTCCCCCGGGCGCAAAGAGAAGCCATCTGATCCCGTCGA        603

Qy    ValMetAspValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThr        464
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Db    GTGATGGATGTCGTCGAATATTTTACTGAGGCTGAATTCCCGGAGCAGGGCCAC        663

Qy    GlnGluGlnIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspVa        484
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Qy    GlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLys        504
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ACCESSION    AR199530
VERSION      AR199530.1    GI:20249604
KEYWORDS     .
SOURCE       Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE    1 (bases 1 to 1617)
  AUTHORS    Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE      Low density lipoprotein binding proteins and their use i
             diagnosing and treating atherosclerosis
  JOURNAL    Patent: US 6355451-A 11 12-MAR-2002;
FEATURES     Location/Qualifiers
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Alignment Scores:
Pred. No.:                3.47e-19     Length:         1617
Score:                    1455.50      Matches:        281
Percent Similarity:       92.86%       Conservative:   18
Best Local Similarity:    87.27%       Mismatches:     13
Query Match:              51.07%       Indels:         10
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US-09-976-740-43 (1-538) x AR199530 (1-1617)
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Qy    280  uAlaAlaAlaArgGlyArgLeuGluArgThrArgLeuGlyAlaLeuAlaLeuPr
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Db    168  GGCGGCGGCGCGGGGCCGCCTGGAGCGCACCCGTCTCGGAGCGGCTTGCGCTGCC

Qy    300  yAspArgProGlyArgAlaProProAlaAlaSerAlaArgProSerArgSerLy
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Db    300
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Score: 1455.50   Matches: 281
Percent Similarity: 92.86%   Conservative: 18
Best Local Similarity: 87.27%   Mismatches: 13
Query Match: 51.07%   Indels: 10
DB: 6   Gaps: 3

US-09-976-740-43 (1-538) x AR374682 (1-1617)

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Qy   477 oGluGlnAlaThrAlaPheGlnGluGlnIleAspGlyLysSerLeuLeu
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3.47e-19   Length: 1617

us-09-976-740-43.rge

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VERSION   AX239568.1   GI:15797248
KEYWORDS
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REFERENCE   1
  AUTHORS   Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
  TITLE   Low density lipoprotein binding proteins and their use in
             and treating atherosclerosis
  JOURNAL   Patent: WO 0164874-A 11 07-SEP-2001;
             Boston Heart Foundation, Inc. (US)
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Alignment Scores:
Pred. No.:   3.47e-19   Length: 1617
Score: 1455.50   Matches: 281
Percent Similarity: 92.86%   Conservative: 18
Best Local Similarity: 87.27%   Mismatches: 13
Query Match: 51.07%   Indels: 10
DB: 6   Gaps: 3

US-09-976-740-43 (1-538) x AX239568 (1-1617)

Qy 221 ProGlnGlnGlnProProProProGlnProGlyGl
Db   6 CCGCAGCAGCAGCAA----------------CAACCCCTAGCGAAGGGTGG

Qy 240 lArgAlaGlyAlaAlaArgProValSerLeuArgProValValArgTyrLe
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Qy 260 ySerGlyGlyAlaGlyArgGluThrArgGlyArgValGlnGlyGlyLeuGl

JOURNAL   diagnosing and treating atherosclerosis
           Patent: JP 2001506983-A 2 29-MAY-2001;
           BOSTON HEART FOUNDATION INC
           PN   JP 2001506983-A/2
           PD   29-MAY-2001
           PF   26-NOV-1997 JP 1998524870
           PR   27-NOV-1996 US   60/031930, 03-JUN-1997 US   60/04€
           ANN M LEES,ROBERT S LEES,SIMON W LAW,ANIBAL A ARONA PC
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FH   Key   Location/Qualifiers

FEATURES   Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:   3.47e-19   Length: 1617
Score: 1455.50   Matches: 281
Percent Similarity: 92.86%   Conservative: 18
Best Local Similarity: 87.27%   Mismatches: 13
Query Match: 51.07%   Indels: 10
DB: 6   Gaps: 3

US-09-976-740-43 (1-538) x BD056444 (1-1617)

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Qy 397 oGlySerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGly
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Qy 417 aSerValAlaThrGlyLeuProProSerProValProLeuProProGlyLys

(left side, rotated sequences read top to bottom)

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aAlaAlaArgGlyArgLeuArgThrArgLeuGlyAlaLeuAlaLeuProArgGl 300
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yGluGluArgValLeuGluLysGluGluLysGluGluLysGluAspAlaProGl 340
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sGluTrpThrProCysGlyGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaPr 397
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gThrAspValLeuThrGlyLeuSerIleArgGluLeuGlyProAlaLeuLeuLysIleTyrGl 517
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Y 538
A 951

RF
BI
LC 444   1617 bp   DNA   linear   PAT 27-AUG-2002
DC low density lipoprotein binding proteins and their use in
    osing and treating atherosclerosis,.
AC 444   GI:22602050
YI 444.1 GI:22602050
XU 0150698-A/2.
SC rea victoria
    rea victoria
    yota; Metazoa, Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
    reidae; Aequorea.
    ases 1 to 1617)
RI A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
    low density lipoprotein binding proteins and their use in

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isHisIleLysValLeuGlnGlnGlyHisPheGluAspAspProAspGlyPheLe  537
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ACCATATCAAGGTGCTGCAGCAGGGTCACTTCGAGGACGATGACCCCGAAGGCTTCCT  947

ly 538
||
GA 951
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: March 13, 2004, 00:37:50
41 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

leic search, using frame_plus_p2n model

March 12, 2004, 19:48:14 ; Search time 852.766 Seconds
                            (without alignments)
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US-09-976-740-43
2850
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BLOSUM62
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Ygapop 10.0 , Ygapext   0.5
Fgapop   6.0 , Fgapext   7.0
Delop   6.0 , Delext   7.0

3373863 seqs, 212409041 residues

hits satisfying chosen parameters: 6747726

ength: 0
ength: 2000000000

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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GN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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is the number of results predicted by chance to have a
er than or equal to the score of the result being printed,
ived by analysis of the total score distribution.

SUMMARIES

N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
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10: geneseqn2004s:*

Query Match	Length	DB	ID	Description
100.0	1614	5	AAH26499	Aah26499 Human low
91.8	12425	5	AAH26495	Aah26495 Human low
91.0	2561	5	AAH26500	Aah26500 Rabbit lo
51.1	1617	5	AAH26488	Aah26488 Rabbit lo
50.9	1617	2	AAV32835	Aav32835 Rabbit lo
44.2	1336	3	AAF21860	Aaf21860 Human bre
41.8	1422	3	AAH26490	Aah26490 Rabbit lo
41.1	1208	2	AAV32838	Aav32838 Human low

	#					ID	Name
	9	1170	41.1	1208	5	AAH26494	Aah26494
	10	1086.5	38.1	1362	5	AAH26489	Aah26489
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c	21	394.5	13.8	110000	4	AAI99682_09	Continuat
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c	27	389	13.6	8438	2	AAQ73500	Aaq73500
	28	388	13.6	110000	4	AAI99682_14	Continuat
	29	388	13.6	110000	4	AAI99683_14	Continuat
c	30	386	13.5	1926	3	AAA50254	Aaa50254
c	31	386	13.5	1926	4	AAF82902	Aaf82902
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c	33	386	13.5	2580	6	AAI64275	Aai64275
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	38	386	13.5	10285	6	ABS66453	Abs66453
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c	41	386	13.5	10596	2	AAX15650	Aax15650
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ALIGNMENTS

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AC   AAH26499;
XX
DT   12-NOV-2001 (first entry)
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DE   Human low density lipoprotein binding protein 2 (LBP-2) DNA.
XX
KW   Low density lipoprotein binding protein 2; LBP-2; LDL; human;
KW   atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis;
KW   ds.
XX
OS   Homo sapiens.
XX
PN   WO200164874-A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006356.
XX
PR   02-MAR-2000; 2000US-00517849.
PR   14-JUL-2000; 2000US-00616289.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR   WPI; 2001-565505/63.
DR   P-PSDB; AAB82806.
XX

low density lipoprotein binding polypeptide for treating,
d/or identifying therapeutic agents for atherosclerosis.

7A; 143pp; English.

equence is that of the coding region of the human gene (see
) encoding novel human low density lipoprotein binding
P-2, see AAB2806). The gene was isolated from a genomic DNA
LBP-2 cDNA as probe. The LBP-2 protein predicted from the
nce differs from that predicted from a cDNA clone (see
that it contains an additional 321 amino acids at its N-
cDNA is a 5' truncation). LBP-2 nucleic acids are among
ucleotides of the invention that encode novel polypeptides
nding to native and methylated LDL. Also claimed are
polypeptides, and biologically active fragments and
them, as well as expression vectors, cells and methods of
LBPs. Methods of determining if an animal is at risk for
is, and methods for evaluating an agent for use in treating
is, and methods for treating a cell having an abnormality in
metabolism of LBP are claimed. Pharmaceutical compositions
. LBP polypeptide or nucleic acid, and vaccine compositions,
med

BP; 243 A; 638 C; 169 T; 0 U; 0 Other;

	2.04e-69
Length:	1614
Matches:	538
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	5
ity:	100.00%

1-538) x AAH26499 (1-1614)

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Qy ProGlnGlnGlnProProProGlnProProGlnProProGlnProGlyGlyGlyA 221
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Qy ArgAlaGlyAlaAlaArgProValSerLeuArgProGluValValAlaArgTyrLeuG 241
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Qy SerGlyGlyAlaGlyGlyArgLeuThrArgGlyValArgGlnValGlyLeuLeuGlyG 261
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Qy AspArgProGlyArgAlaProProAlaAlaSerArgAlaArgProSerArgSerLysAr 301
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Db GACAGGCCCGGACACGGGCCCGGCCCGGCCCGTCTCGCAGCAAGAC 901

Qy GlyGluGluArgValLeuGluLysGlnGluGluGluLysGluGluAspAspGluAr 321
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Qy GluAspAspValSerGluGlySerGluvalProGluSerAspArgProAlaGlyAl 341
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Qy ThrProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGlySe 381
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Qy ThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerVa 401
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Db ACAGCTTTCCAAGACAGCAGAAATTGATGGCAAATCTTTGCTGCTCATGCAGCGAC 1441

Qy ValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHi 501
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Qy LysValLeuGlnGlnHisPheGluAspAspAspProAspGlyPheLeuGly 5 521
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RESULT 2
AAH26495
ID AAH26495 standard; DNA; 12425 BP.

(first entry)

ensity lipoprotein binding protein 2 (LBP-2) gene.

, lipoprotein binding protein 2; LBP-2; LDL; human;
osis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;

s.

Location/Qualifiers
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    /*tag= j

-A2.

; 2001WO-US006356.

; 2000US-00517849.
; 2000US-00616289.

TON HEART FOUND INC.

ees RS, Law SW, Arjona AA;

65505/63.
82806.

d low density lipoprotein binding polypeptide for treating,
and/or identifying therapeutic agents for atherosclerosis.

Fig 23; 143pp; English.

sequence is that of genomic DNA encoding novel human low
oprotein binding protein 2 (LBP-2, see AAB82806). The DNA was
om a human genomic library by screening with LBP-2 cDNA (see
The open reading frame spans 5 exons. Human LBP-2 nucleic
nong claimed polynucleotides of the invention that encode
eptides, termed LBPs, capable of binding to native and
LDL. Also claimed are isolated LBP polypeptides, and
y active fragments and analogues of them, as well as
vectors, cells and methods of producing the LBPs. Methods of
if an animal is at risk for atherosclerosis, methods for
an agent for use in treating atherosclerosis, and methods for
cell having an abnormality in structure or metabolism of LBP
. Pharmaceutical compositions comprising an LBP polypeptide or
d, and vaccine compositions, are also claimed

425 BP; 2563 A; 3702 C; 3566 G; 2594 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:
Score: 1.35e-62
Percent Similarity: 2616.50
Best Local Similarity: 69.16%
Query Match: 69.16%
DB: 91.81%
                             5

Length: 12425
Matches: 536
Conservative: 0
Mismatches: 2
Indels: 239
Gaps: 4

US-09-976-740-43 (1-538) x AAH26495 (1-12425)

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Qy   21 AlaAlaSerSerSerAlaAlaSerProHisThrGlnGluTrpIleLeuAspTh:
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2892 GCCGCCTCGTCGTCCGCCGCTTCCCCGCACTACCAAGAGTGGATCCTGGACAC(

Qy   41 SerLeuArgSerArgLysAlaArgProAspLeuGluArgIleCysArgMetVa.
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Db   2952 TCGCTGCGCTCGCGCAAGGCGCGGCCGGACCTGGAGCGCATCTGCCGGATGGT(

Qy   61 ArgHisGlyProGluProGlyArgThrArgAlaGluLeuGluLysLeuIleGlı
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Db   3012 CGGCACGGGCCCGGAGCCCGGAGCGCACGGCGCCGGAGCTCGAGAAACTGATCCA(

Qy   81 AlaValLeuArgValSerTyrLysGlySerIleSerTyrArgAsnAlaAlaAr(
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Qy   101 ProProArgArgGlyAlaThrProAlaGlyAlaProAlaProArgGlyValAl;
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Db   3132 CCGCCCCGGCGCGGAGCCACCCCGCCGGCCCCGGCGCCCCCGCGGGGGC(

Qy   121 AlaAlaAlaAlaAlaAlaProProThrProAlaProProProProAlaProProA
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Db   3192 GCCGCCGCCGCCGCCGCCCCGCCCACGCCCGCACCGCCCCCGCCCCCG(

Qy   141 AlaAlaAlaAlaAlaProAlaAlaArgAlaProArgAlaAlaAlaAlaAlaThrAl;
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3252 GCCGCCGCCGGCCCCGCCCCCGGGCGCCCGCGGGCCGGCCCCGCCACAGC(

Qy   161 SerProGlyProAlaGlnProGlyGlyProAlaGlnArgAlaGlnArgAlaProLeuAl;
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   3312 TCGCCTGGCCCCGCAGCCCGGCGGCCCCGGCGCAGCGGCCGGGCCCCTGGC(

Qy   181 ProProAlaProAlaAlaProAlaValAlaProAlaProProGlyProArgArg
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Db   3372 CCGCCCGCGCCAGCCGCTCCCCGGCGGTGGCGCCCGGCCCGGCGGCGC(

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Qy   221 ProGlnGlnGlnProProProGlnProGlnProProGluProProGluGly
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Db   3492 CCACAGCAGCAGCCGCCGCCGCCAGCCACAGCCGCCGCCCGAGGGGGGC

Qy   241 ArgAlaGlyAlaAlaAlaArgProValSerLeuArgGluValValArgTyrLeu
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Db   3552 CGGGCCGGCGGCGCCGCGCCCGTGAGCCTGCGGGAAGTCGTGCGCTACCTC

Qy   261 SerGlyGlyValAlaGlyArgLeuThrArgGlyArgValGlnGlyLeuLeuGlu
          |||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   281 AlaAlaArgGlyArgLeuGluArgThrArgLeuGluLeuAlaLeuPro
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   3672 GCGGCGGCTTCGAGCGCACCCGTCTCGGAGCGCTCCTCGGAGCGCTACCTC

Qy   301 AspArgProGlyValArgProAlaAlaSerAlaAlaProSerArg------
          |||||||||||||||||||||||||||||||||||

Qy   477 roGluGlnAlaThrAlaPheGlnGlu------------
              ||||||||||
Db   4871 CGGAGCAGGCGACAGCTTCCAAGA-GCAGGTGAGTTCCAGCCCAGGACTACA(

Qy   485 ----------------
Db   4930 CAGACACAGAGGGCCCCTGGGATGTGCCCTGATCCGGCTTCTCTGTCCTC

Qy   486 --GlnGluIleAspGlyLysSerLeuLeuMetGlnArgThrAspValLeuT
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db   4990 CCCAGGAAATTGATGGCAAATCTTTGCTCATGCAGCGCACAGATGTGCTCA(

Qy   505 euSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLysValLe
          ||||||||||||||||||||||||||||||||||||||||||||
Db   5050 TGTCCATCCGCCTCGGGCCAGCCCTGAAAATCTACGAGCACCACATCAAGGTGCT

Qy   525 lnGlyHisPheGluAspAspAspProGlyPheLeuGly 538
          ||||||||||||||||||||||||||||||||||||
Db   5110 AAGGGCCACTTTGAGGATGATGACCCCGATGGCTTCTTAGGC 5150

RESULT 3
AAH26500
ID   AAH26500 standard; cDNA; 2561 BP.
XX
AC   AAH26500;
XX
DT   12-NOV-2001 (first entry)
XX
DE   Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA.
XX
KW   Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit;
KW   atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis;
KW   ss.
XX
OS   Oryctolagus cuniculus.
XX
FH   Key   Location/Qualifiers
FT   CDS   246..1928
FT   /*tag= a
XX
PN   WO200164874-A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006356.
XX
PR   02-MAR-2000; 2000US-00517849.
PR   14-JUL-2000; 2000US-00616289.
XX
PA   (BOST-) BOSTON HEART FOUND INC.
XX
PI   Lees AM, Lees RS, Law SW, Arjona AA;
XX
DR   WPI; 2001-565505/63.
DR   P-PSDB; AAB82807.
XX
PT   New isolated low density lipoprotein binding polypeptide for tre
PT   diagnosing and/or identifying therapeutic agents for atheroscler
XX
PS   Claim 4; Fig 2A; 143pp; English.
XX
CC   The present sequence is that of cDNA encoding novel rabbit low d
CC   lipoprotein binding protein 1 (LBP-2, see AAB82807). The CDNA wa
CC   isolated following screening of a rabbit cDNA library for clones
CC   LBPs that bound to both native low density lipoprotein (LDL) and
CC   LDL. The invention provides claimed polynucleotides encoding nov
CC   polypeptides which are capable of binding to native and methylat
CC   the isolated polypeptides, termed LBPs, and biologically active
CC   and analogues of them, as well as expression vectors, cells and
CC   of producing the LBPs. Also claimed are methods of determining i
CC   animal is at risk for atherosclerosis, methods for evaluating an
CC   for use in treating atherosclerosis, and methods for treating a

---

Qy   AGGCCCGGACGGGCGCGCCGGCCGCCAGCGCCGTCTCCGCAGCAAGGTGAGC 3791
         ------------- 316

Qy   CCGGGGAGCGCGGGGGCGCGCCGGCGGTGGGCAGGTGCGGGCGAAGTTGGTGGCGGGGGC 3851
         ------------- 316

Qy   AGTCCCGGGAGGAACTGGGTGGGGGGTGGCTGGGGGCTTGGCGCGCGTTTCGTGCGGGG 3911
         ------------- 316

Qy   GGTGCGTGGTGGTCGACCTTGGCAAGTGATTGAATTCCCGGAGCCTCAGTTTCCTCCGCT 3971
         ------------- 316

Qy   AACGCGGTTTAATAACAGTAGGCGACCCCCTTGGGGTTGTTGAGCGAGTTTAGTAAGAAT 4031
         ------------- 316

Qy   GTTGTGCGAGGGCTTTAGTTAACACAGAGCCCTGCACGGAGTGAATGCGTAAAAGTTA 4091
         ------------- 316

Qy   CGTATTGTTCTTAAAGGTGGAATCGGTTCCTCCTCCCACCGCCCGGACGCCCACAGT 4151

Qy   ----------------SerLysArg 319
                         |||
Qy   GGTCGGATTAGAACAGCTACTACTAATTTGCATGCTTCTCTCCGGCTCCAG-AGA 4210

Qy   339 GlyGlyGluGlyArgValLeuGluLysGluGluGluGluAspAlaAspGluAspGluAsp
             ||||||||||||||||||||||||||||||||||
Db   GGAGAAGGAGAGTACTTGAGAAGAAGAAGAGGAAGATGATGAAGATGAAGAT 4270

Qy   359 GluAspAspValSerGluGlyLysSerGluValProGluSerAspArgProAlaGlyAla
         |||||||||||||||||||||||||||||||||||||||
Db   GAAGATGATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCCTGCAGGTGCC 4330

Qy   379 HisHisGlnLeuAsnGlyGlyLuGluArgGlyTyrProGlnSerAlaLysGluArgValLysGlu
         ||||||||||||||||||||||||||||||||||||||||
Db   CACCACCAGCTTAACGGCGGAGGCGGGGACCTCAGAGTGCCAAGGAGGGGTCAAGGAG 4390

Qy   399 ThrProCysGlyProHisGlnGlyGlnAspGluLuArgGlyTyrArgGlyProAlaProGlySer
         ||||||||||||||||||||||||||||||||||
Db   ACCCCCTGCGGACCGCCACCAGGGCCAGGATGAAGGGCGGGGGCCAGCCCCGGCAGC 4450

Qy   416 ThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThr----------
         ||||||||||||||||||||||||
Db   ACCCGCCAGGTGTTCTCCATGGCAGCCATGAACAACAAGGAAGGGGAACAGGTAAGGAT 4510

Qy   416
Db   TCTGGGTGGGGGAAGAGTGCTAGGTGGAGAGAGTGAGAGGAGAACTCAGCCCGAAGACAAAGCCAAAG 4570

Qy   429 ----AlaSerValAlaThrGlyLyProGlyAspSerProProVa
              ||||||||||||||||
Db   --AlaSerValAlaThrGlyLyProGlyAspSerProProVa 429
Db   GGTGTTTTTTTCCTTCCGAGCTTCGTTGCCACCGGGGCCAGACTCCCCGTCCCCGT 4630

Qy   449 cLeuProProGlyLyProGlyAlaLeuProGlyValAlaAspGlyThrProPheGlyCysPr
         |||||||||||||||||||||||||
Db   TTTGCCCCAGGCAAACCAGCCCTACCTGGGGCCGACCCCCCTTTGGCTGTCC 4690

Qy   449
Db   AGTTGGGGTATTGGAGACATGGGGGTGCTGCTCAGTGTGTGTACGCCAGAGAGA 4750

Qy   457 ----------------ProGlyArgLyGluLyProS
                          ||||
Db   ProGlyArgLysGluLysProS 457
Db   CCGTGTTCACTGTGTCTGTTTGTTTTGATGCAGTCCCGGCGCAAAGAGAGCCAT 4810

Qy   477 spProValGluTrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheP
         |||||||||||||||||||||
Db   ATCCCCGTCGAGTGGACCGTGATGGATGTCGTCGAATATTTTACTGAGGCTGGATTCC 4870

bnormality in structure or metabolism of LBP. Pharmaceutical
s comprising an LBP polypeptide or nucleic acid, and vaccine
s, are also claimed

61 BP; 372 A; 937 C; 879 G; 373 T; 0 U; 0 Other;

```
                    2.13e-62
                    2594.00
ty:      94.20%
arity:   91.12%
         91.02%
         .5
```

```
Length:        2561
Matches:        503
Conservative:    17
Mismatches:      16
Indels:          16
Gaps:             8
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(1-538) x AAH26500 (1-2561)

```
Qy  tAlaGlyProProAlaLeuProProGluThrAlaAlaAlaAlaThr---Ala   19
         |||||||||||||||||||||||||||||||||||||||||||
Db  GGCGGGGGCCCCCGGCCCTACCCCCGGGACACGGCGGCGGCGGCCACCGGCGCG  305

Qy  aAlaAlaSerSerAlaAlaSerProHisTyrGlnGluTrpIleLeuAspThrIle   39
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  CGCCGGCCTCGTCGTCGCCGCGTTCCCGCACTACCAAGAGTGGATTCTGGACACCATC  365

Qy  pSerLeuArgSerArgGlyAlaArgProAspLeuGlyArgIleCysArgMetValArg   59
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  CTCGCTCGCCTCGCGCAAGGCGCGGGCCGGACCTTGGAGCGCATCTGCCGGATGGTGCGG  425

Qy  gArgHisGlyProGluGluProGlyArgThrArgAlaGlyLeuGluLysLeuLeuGlnGln   79
         |||||||||||||||||||||||||||||||||| :::|
Db  GCGGCACGGCCCCGGAGCGCACGGCGCCGAGCTCGGAGAAACTGATCCAGCAG  485

Qy  pAlaValLeuArgValSerTyrLysGlySerIleSerTyrArgAsnAlaAlaArgVal   99
         |||||||||||||||||||||||||||||||
Db  CGCCGTGTCCTCAGCTACAAGGGGAGCCATCTCGTACCCGCAACGCGGCGCGCGTC  545

Qy  1ProProArgArgGlyAlaThrProProAlaProProArgAlaProArgGlyAlaPro  119
         ||||||||||||||||||||||||||||||||||||||||||
Db  CCCGCGGGGCGGGGAGCCACCCCGCCGGCCCCGCCGCGCCCCGGGGGGCCCC  605

Qy  aAlaAlaAlaAlaAlaAlaProProProThrProAlaProThrProAlaProAlaPro  139
         |||||||||||||||||||||||||||||||||||
Db  GCCGCGCGCCGGCGCCCGGCCCCAGCCCCGCGCCGCCCGCGCCCCGGCCCC  659

Qy  1---AlaAlaAlaAlaProAlaArgAlaProAlaPro-----AlaAlaAlaAlaAla  156
            |||||||||||||||||||||||||||||||
Db  ---GCCGCGCGCCGGCGCCCCGCCCCGGCGCCCGGCGCCGCCGGGCCGCCGCCGCC  719

Qy  1AlaProProSerProGlyProAlaGlnProGlyProArgAlaGlnAlaGlnAlaAlaPro  176
         |||||||||||||||||||||||||||||||||||||||
Db  AGGCGCCCCCCTCGCCCCGGCCCCGGAGCCCCGCCCCGCAGCGCGGGCCGCGCCC  779

Qy  1AlaAlaProProProAlaProAlaAlaProAlaProAlaValAlaAlaProProAlaGlyPro  196
         |||||||||||||||||||||||||||||||||||||
Db  GGCCCCGGCCCCGCCCCGCCGCCCGCCCGGCGCCCCCGGGGGGCCGCCGCCCG  839

Qy  1ArgAlaProAlaProPro-----AlaValAlaAlaArgGluProLeuProProPro  214
         |||||||||||||||          ||||||||||||||||||||||||
Db  CGGGGCCCCCCCCGCGCCGGCGCCCCGGGCCCCCTGCCCCGGAGTCGCCCTGCCCCG  899

Qy  1GlnProProAlaProProGlnGlnGln------ProProProPro  229
         ||||||||||||||||||||            |||||||||
Db  CAGCCGCCGGCGCGCCGGCCACAGCAGCAGCAGCGCGCCGCCGCCGCCACGCGCCGCCAG  959

Qy  1ProGlnProProProGluGlyGlyAlaValAlaArgAlaGlyGlyAlaAlaAlaArgProVal  249
         |||||||||||||||||||||||||||||||||||||||||||
Db  CCCACGCCGCCCGCCGGAGGGGGGCGCGGCGGGGCGCCCGGCCGCCGGGCCGGGCCCCGTG  1019

Qy  1LeuArgGluGlyValValalArgTyrLeuGlySerGlyGlyGlyValAlaGlyGlyArgLeuThr  269
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  CTGCGGGGAAGTCGTGCGCTACCTCGGGGGTAGCAGGCGGCCTGCCGGCCGCCGCCCTGACC  1079

Qy  1GlyArgValGlnGlyLeuLeuGluGluGluAlaLeuAlaAlaAlaArgGlyArgLeuGluArg  289
```

```
Db  1080  CGCGGCGGCGTGCAGGTCTGCTGCTGGAAGAGAAGAGAGGAGGCGGCGGCGGCGGCGGCGGCGCT(
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   290  ThrArgLeuGlyAlaLeuAlaLeuProArgGlyAspArgProGlyArgProGlyArgAlaPro
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1140  ACCCGTCTCGGAGCGCTTGGCGTGCCGGGACAGGCCCGAGGGGGCC
Qy   310  AlaSerAlaArgProSerArgSerLysArgGlyGlyValGlyGluArgValLeuGlu
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1200  GCCAGCGCCCGCCGCGCGGAACAAGAGACAGCTGGCCGAGGAGGCGAGTGCTTGA
Qy   330  GluGluGluAspAspAspGluAspGluAsp-----ValSer
             ::::::::::::: |||
Db  1260  GAGGAGGAGGAGGAGGAGGAGAAGACGACGAGACGACGACGACGTCGTGTCC
Qy   348  SerGluValProGluSerAspArgProAlaGlyAlaGlnHisHisGlnLeuLeuAsn
             |||||||||||||||||||||||||||||||||||||||||||||
Db  1320  TCGGAGGTGCCCGAGAGCGAGATCGTCCCGCGGGTGGGCCAGCATCACCAGCTGAAT
Qy   367  GluArgGlyProGlnSerAlaLysGluArgValLysGluTrpThrProCysGly
             |||||||||||||||||||||||||||||||||||||||||||||
Db  1380  GAGCGCGGCCCCCAGACCGCCAAGGAGGCGGGCCAAGGAGTGCTCGCTGTGTGGC
Qy   387  GlnGlyGlnAspGluValArgGlyProAlaProGlySerGlyThrArgGlnVal
             ::: ||||||||||||||||||||||||||||||||||||||||||||
Db  1440  CCTGGCTGCCAGGAGGAAGGGCGGGGGCCGGCCCGGCCAGTGGCACCCGCCAGGTG
Qy   407  MetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThrGlyPheProAsp
             |||||||||||||| :::|  ||| :::||||||||||||||||||
Db  1500  ATGGCGGCCTTGAGTAAGGAGGGGGGATCAGCCTCTTCGACCACCACCGGGCCTGAC
Qy   427  SerProValProLeuProProGlyProLysProAlaLeuProGlyAlaAspGlyThr
             ||||||||||||||||||||||||||||||||||||||||||||
Db  1560  TCCCCGGTGCCTTTGCCCCCGGGAAGCCAGCCCTTCCCAGGAGCGCGATGGGACC
Qy   447  GlyCysProProGlyTyrArgGlyGluLysLysProSerAspProValGlyTrpThrVal
             ||| :::||||||||||||||||||||||||||||||||||||||||||||||
Db  1620  GGCTGCCCTGCCCGGCTACAGAGGCGCAAAGAAGAGCCGGCAGACCCGTGGAGTGGACAGTC
Qy   467  ValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThrAlaPheGln
             |||||||||||||||||||||||||||||||||||||||||||||
Db  1680  GTCGTGGAGTACTTCACCGAGGCGGGCTTCCCTGAGCAAGCCACGGCTTTCCAG
Qy   487  GluIleAspGlyLysSerLeuLeuMetGlnArgThrAspValLeuThrGly
             ||||||||||||||||||||||||||||||||||||||||||||
Db  1740  GAGATCGACGGCAAGTCCCTGCTCATGCAGCGCACCGATGTCCTCACCGGC
Qy   507  IleArgLeuGlyProAlaLeuLysIleTyrGluHisHisLysValLeuGln
             ||||||||||||||::: |||||||||||||||||||||||||||||
Db  1800  ATCCGCCTGGGCCAGCGTTGAAAATCTATGAGCACCATATCAAGGTGCTGCAG
Qy   527  HisPheGluAspAspAspProAspGlyPheLeuGly  538
             ||||||||||||||||:::||||||||||||
Db  1860  CACTTCGAGGACGATGACCCGAAGGCTTCCTGGGA  1895
```

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FT   /tag= a
FT   /partial
FT   /note="includes in-frame stop codon at nucleotides
FT   28..30"
XX

XX   A2.

XX   2001WO-US006356.

XX   2000US-00517849.
XX   2000US-00616289.
XX

XX   DN HEART FOUND INC.

XX   es RS,  Law SW,  Arjona AA;

XX   5505/63.
XX   2798.
XX

     low density lipoprotein binding polypeptide for treating,
     d/or identifying therapeutic agents for atherosclerosis.

     g 11; 143pp; English.

     sequence is that of cDNA encoding a portion (see AAB82798) of
     low density lipoprotein binding protein 2 (LBP-2). The cDNA
     following screening of a rabbit cDNA library for clones
     s that bound to both native low density lipoprotein (LDL) and
     A full-length sequence for LBP-2 is given in AAH26500. The
     ovides claimed polynucleotides encoding novel polypeptides
     pable of binding to native and methylated LDL, the isolated
     termed LBPs, and biologically active fragments and
     them, as well as expression vectors, cells and methods of
     a LBPs. Also claimed are methods of determining if an animal
     or atherosclerosis, methods for evaluating an agent for use
     atherosclerosis, and methods for treating a cell having an
     in structure or metabolism of LBP. Pharmaceutical
     comprising an LBP polypeptide or nucleic acid, and vaccine
     , are also claimed

     7 BP; 289 A; 513 C; 530 G; 285 T; 0 U; 0 Other;
```

```
/:        7.73e-32        Length:         1617
P:        1455.50         Matches:        281
Sc        92.86%          Conservative:   18
Ee        87.27%          Mismatches:     13
Qu        51.07%          Indels:         10
DB        5               Gaps:           3
```

```
US   (1-538) x AAH26488 (1-1617)

Qy   GlnGlnGlnProProProGlnProGlnPro-ProGluGlyGlyAlaVa 240
     ||||||||||||||
Db   CAGCAGCAGCAA-----------------CAACCGTAGCCGAAGGGTGGCGCGGC 47

Qy   AlaGlyGlyAlaAlaAlaArgProValSerLeuArgGluValValArgTyrLeuGlyGl 260
     ||||||||||     |||||||||||||||||||||||||||||||||||||||||||
Db   GCCGGCGGCGCCGGCGGCGCCCGTGAGCCTGGCGGAAGTCGTGCGCTACCTCGGGGG 107

Qy   GlyAlaGlyLyGlyArgLeuThrArgGlyArgValArgGlnGlyLeuLeuGluGluGl 280
     ||||||||||||||||||||||||||||||||||||||||||||||
Db   CAGGCGGCGGCCTGGCGCGGCCGCCTGACCCGGCGGGCCGTGCAGGGTCTGCTGGAAGAGGA 167

Qy   AlaAlaAlaArgGlyArgGluArgThrArgLeuGlyAlaLeuAlaLeuProArgGl 300
     |||||||||||||||||||||||||||||||||||||||||||||
Db   GGCGGCGGCGGGCCGGGCCACCCGTCTCGGAGCGCTTGCCGCTGCCCCGCCG 227

Qy   ArgProGlyArgAlaProAlaAlaSerAlaArgProSerArgSerLysArgGl 320
     |||||||||||||||||||||     :::||||||||||||||||||
Db   CAGGCCCGGACGCGGGGCGCCACCGGCCCCAGCGCCCGGCGGGCCGGGAACAAGAGAGC 287
```

```
Qy   320  yGlyGluGluArgValLeuGluLysGluGluGluGluAspAspAspGluAspGlu
          ::::||:::||||||||
Db   288  TGGCGGAGGAGCGAGTGCTTGAAAAGAGGAGGAGGAGGAGGAGGAGGAAGACGAC

Qy   340  uGluAspAsp-----ValSerGluGlySerGluValProGluSerAspArgPro
          :::||||              ||||||||||||||||||||||||||||
Db   348  CGAGGACGACGTCGTGTCCGAGGGCTCGGAGGTGCCCGAGAGCGATCGTCCC

Qy   358  yAlaGlnHisHisGlnLeuAsn---GlyGluArgGlyProGlnSerAlaLysGlu
          |||||||||||||:::|||             ||||||||::::||||||||||
Db   408  TGCCAGCATCACCAGCTGAATGGCGGCGGAGCGCGGCCCCAGACCGCCAAGGAG

Qy   377  lLysGluTrpThrProCysGlyTyrProHisGlnGlnAspGlyArgGlyPro
          |||||||:::            ||||||||||||||||||::||||||||||
Db   468  CAAGGAGTGGTGCGCTGTGTGGGCCCCACCCTGGCCAGGAGGAGGAAGGGCGGGGGCCG

Qy   397  oGlySerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGly
          |||||::||||||||||||||||||||||||||||::::||||||||
Db   528  GGGCAGTGGCCAGCCGCCAGGTGTTCTCCATGGCCGCCATGAACAAGGAGGGGGGA

Qy   417  aSerValAlaThrGlyProAspSerProSerProValProLeuProProGlyLys
          |||||              ||||||||||||||||||||||||||||||||
Db   588  CTCTTCGACCACCGCGGCCTGACTCCCCGTCCCCGGTGCCTTGCCCCCGGAAG

Qy   437  aLeuProGlyAlaAspGlyThrProPheGlyTyrProGlyGlyProGlyLysGluLys
          ||||              ||||||||||||||||||||||||||||||||||||
Db   648  CCTCCCAGGAGCCGATGGGACCCCTTGGCTGCCTGCCCTGCCCGGGGCCAAAGAGAAG

Qy   457  rAspProValGluTrpThrValMetAspValValGluThrPheThrGluAlaGly
          :|||              ||||||||||||||||||||||||||||||||||||||
Db   708  AGACCCCGTGGAGTGGACAGTCATGGACGTCGTGGAGTACTTCACCGAGGCGGGC

Qy   477  cGluGlnAlaThrAlaPheGluGlnLeuIleAspGlyLysSerLeuLeuLeu
          |||||||||||||||||||||||||||||||||||||||||||||
Db   768  TGAGCAAGCCACGGCTTTCCAGGAGCAGCAGGAGATCGACGGCAAGTCCCTGCTCTC

Qy   497  nArgThrAspValLeuThrGlyLeuSerIleArgGlyProAlaLeuLysIle
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   828  GCGCACCGATGTCCTCACCGGCCTGTCCATCCGCGGCCCGGGGCCCAGCGTTGAAAATC

Qy   517  uHisHisIleLysValLeuGlnGlnGlyHisPheGluAspAspArgProAspGly
          ||||||||||||||||||||||||||||||||||:::||
Db   888  GCACCATATCAAGGTGCTGCAGCAGGGTCACTTCGAGGACGATGACCCGGAAGGC
```

```
Qy   537  uGly 538
          ||||
Db   948  GGGA 951
```

```
RESULT 5
AAV32835
ID   AAV32835 standard; cDNA; 1617 BP.
XX
AC   AAV32835;
XX
DT   09-NOV-1998  (first entry)
XX
DE   Rabbit low density lipoprotein binding protein LBP-2 cDNA.
XX
KW   Low density lipoprotein binding protein; LDL binding protein 2;
KW   receptor; rabbit; atherosclerosis; diagnosis; therapy; vaccine;
XX
OS   Oryctolagus cuniculus.
XX
FH   Key              Location/Qualifiers
FT   CDS              1..954
FT                    /tag= a
FT   misc_feature     156..1617
FT                    /tag= b
FT                    /note= "Claim 5"
FT   misc_feature     156..954
FT                    /tag= d
FT                    /note= "Claim 6"
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     /*note= "Claim 5"
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e    313..360
     /*tag= e
     /*note= "Claim 18"
e    361..396
     /*tag= g
     /*note= "Claim 20"
e    631..660
     /*tag= h
     /*note= "Claim 21"
1.

;    97WO-US021857.

;    96US-0031930P.
;    97US-0048547P.

TON HEART FOUND INC.

ees RS,  Law SW,  Arjona AA;

22455/28.
49038.

d encoding low density lipoprotein binding proteins and
tors - transformed cells, proteins, and modulators of binding,
treatment and diagnosis of atherosclerosis and for identifying
risk.

g 11; 47pp; English.

lone codes for novel rabbit low density lipoprotein (LDL)
tein LBP-2 (see AAW49038). It was isolated by functional
f a cDNA library, produced from balloon-deendothelialised
bit abdominal aorta mRNA, for clones encoding LBPs able to
ative and methyl LDL, cDNA clones (see AAV32834-39) and
bit and human LBPs (see AAW49037-42) are claimed. An
in an aspect of LBP metabolism or structure is diagnostic of
atherosclerosis. The invention provides: methods for
if an animal is at risk for atherosclerosis (e.g. for
eening); methods for treating atherosclerosis (including gene
ing e.g. LBP polypeptides to bind LDL and thereby prevent
atherosclerotic plaque; and methods for treating a cell
normality in LBP structure or metabolism. Pharmaceutical and
positions are also provided, as well as recombinant vectors
lls used to produce recombinant LBP

7 BP; 290 A; 513 C; 529 G; 285 T; 0 U; 0 Other;

      1.12e-31          Length:           1617
      1449.50           Matches:          280
y:    92.55%            Conservative:     18
rity: 86.96%            Mismatches:       14
      50.86%            Indels:           10
      2                 Gaps:             3

(1-538) x AAV32835 (1-1617)

pGlnGlnGlnProProProGlnProPro-ProGluGlyGlyAlaVa 240
|||||||||||             |||||||||  ||||||||||
GCAGCAGCAGCAA-----------CAACCCGCTAGCCGAAGGGTGGCGCGGC 47

gAlaGlyGlyAlaAlaArgProValSerLeuArgGluValValAlaArgTyrLeuGlyGl 260
||||||||||||||   |||||||||||||||||||||||||||
```

```
Db   48   GCGGGCGCGGCGCGCCCGGCGCGCGCCCGTGAGCGCTGCGCGGAAGTCGTGCGCTACC

Qy   260  ySerGlyGlyAlaGlyGlyArgLeuThrArgGlyArgValGlnGlyLeuLeuG
Db   108  TAGCAGCGGCGCTGCGCGGCCCCTGACCCGGCCGGGTCGTGGA

Qy   280  uAlaAlaAlaArgGlyArgLeuGluArgThrArgLeuGlyAlaLeuAlaLeuP
Db   168  GGGCGGCGGCCGCGGGCCGCCTGGAGCGCACCCGTCTCGGAGCGCTTGCGCTGC

Qy   300  yAspArgProGlyArgAlaProAlaSerAlaArgProSerArgSerL
Db   228  GGACAGGCCCCGACGGGCGCCACCGGCGCCCGCGCGGCGGAACA

Qy   320  yGlyGluGlyArgValLeuGluLysGluGluGluAspAspAspGluAspG
Db   288  TGGCGAGGAGGCGGAGTGCTTGAAAAGGAGGAGGAGGAGGAAGACGA

Qy   340  uGluAspAsp-------ValSerGluGlySerGluValProGluSerAspArgP
Db   348  CGACGACGACGACGTCGTGTCCAGGGTCTCGGAGGTGCCCGAGGAGCGGATCGTCC

Qy   358  yAlaGlnHisHisGlnLeuAsn---GlyGluArgGlyGlnSerAlaLysG
Db   408  TGCGCAGCATCACCAGCTGAATGGCCGGCGAGCGCGGCCCGAGACCCGCCAGGA

Qy   377  lLysGluTrpThrProCysGlyTyrThrProHisGlnGlnAspGluGlyArgGlyYP
Db   468  CAAGGAGTGGTCGCTGTGTGGCCCCCACCCTGGCCAGGAGCAGGAAGGGCGGGGGCC

Qy   397  oGlySerGlyThrArgGlnValPheSerMetAlaAlaMetAlaAsnLysGluGlyG
Db   528  GGGCAGTGGCACCCGCCAGGTGTTCTCCATGGCGGCCTTGAGTAAGGAGGGGGC

Qy   417  aSerValAlaThrGlyProAspSerProSerProValProLeuProProGlyLy
Db   588  CTCTTCGACCACCGGCCTGACTCCCCGTCCCGGTGCCTTTGCCCCCCCGGGAA

Qy   437  aLeuProGlyValAlaAspGlyThrProPheGlyCysProPheGlyArgLysGluLy
Db   648  CCTCCCAGGAGCCCATGGAGGACCCCCTTTGGCTGCCCTGCCGGGCGCAAAGAGAA

Qy   457  rAspProValGluTrpThrValMetAspValValAlaGluTyrPheThrGluAlaG
Db   708  AGACCCCGTGGAGTGGACAGTCATGGACGTTCGTGGAGTACTTCACCGAGGACGG

Qy   477  oGluGlnAlaThrAlaPheGlnGluGlnLeuIleAspGlyLysSerLeuLeuLe
Db   768  TGAGCAAGCCACGGCTTTCCAGGAGCAGGAGATCGACGCAAGTCCCTGCTGCT

Qy   497  nArgThrAspValLeuThrGlyLeuSerIleLeuArgLeuGlyProAlaLeuLysIl
Db   828  GCGCACCGATGTCCTCACCGGGCTGTCCATCCCGCCTGGGCCAGCGTTGAAAAT

Qy   517  uHisHisIleLysValLeuGlnGlnGlyHisPheGluAspGluAspAspAspAspGl
Db   888  GCACCATATCAAGGTGCTGCAGCAGGGTCACTTCGAGGACGATGACCCGGAAGG

Qy   537  uGly 538
          |||
Db   948  GGGA 951
```

RESULT 6
AAF21860
ID   AAF21860 standard; DNA; 1336 BP.
XX
AC   AAF21860;
XX
DT   27-MAR-2001 (first entry)
XX
DE   Human breast and ovarian cancer associated antigen gene SEQ ID
XX
KW   Human; breast cancer; ovarian cancer; cytostatic; immunosuppres

surpprotective; antiviral; antiallergic; hepatotropic;
; antiinflammatory; antiulcer; vulnerary; anticonvulsant;
l; antifungal; antiparasitic; cardiant; immune disorder;
sease; allergy; autoimmune haemolytic anaemia;
tyroiditis; diabetes mellitus; Crohn's disease;
erosis; rheumatoid arthritis; ulcerative colitis;
ar disorder; wound healing; neurological disease; ds.

.

al.

2000WO-US005881.

99US-0124270P.

N GENOME SCI INC.

lben SM;

1515/58.
9957.

east and ovarian cancer associated gene sequences and the
encoded by these genes, useful in the prevention, treatment
s of cancer, immune disorders, cardiovascular disorders and
diseases.

a 670-671; 1299pp; English.

F21614 - AAF22031 represent DNA sequences encoding human
58711 - AAB59128. The DNA and protein sequences are
ith breast and ovarian cancer. Included in the invention are
F22032 - AAF22040 and AAB59129 which are used in the
d characterisation of the DNA and protein sequences of the
he breast and ovarian cancer associated DNA, protein, agonist
c sequences exhibit cytostatic; immunosuppressive; nootropic;
ive; antiviral; antiallergic; hepatotropic; antidiabetic;
cory; antiulcer; vulnerary; anticonvulsant; antibacterial;
antiparasitic and cardiant activity. The polynucleotide and
ences are used in the diagnosis of cancer, particularly
varian cancer. The nucleic acid sequences, proteins, agonists
may also be used in the diagnosis, prevention and treatment
borders e.g. Addison's disease, allergies, autoimmune
haemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
ciple sclerosis, rheumatoid arthritis and ulcerative colitis;
ar disorders such as myocardial ischaemias; wound healing;
diseases such as cerebral anoxia and epilepsy; and
iseases

5 BP; 318 A; 396 C; 348 G; 270 T; 0 U; 4 Other;

1.28e-26	Length:	1336
1260.00	Matches:	234
/: 97.51%	Conservative:	1
city: 97.10%	Mismatches:	6
44.21%	Indels:	0
3	Gaps:	0

(1-538) x AAF21860 (1-1336)

```
ArgGlyAspArgProGlyArgAlaProProAlaAlaSerAlaArgProSerArgSer 317
| |||::::                                                        
CGCGGGGACAAGGCCCGGACGGNGCCGCCGCCCAGCGCCCGTCTCGCAGC 60

ArgGlyGlyGluGluArgValLeuGlyLysGluGluGluGluAspAspAspGluAsp 337
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GAGGTGGAGAAGAGCGAGTACTTGAGAAAGAAGAAGATGATGATGAAGAT 120

ArgGlyAspAspValSerGluGlySerGluValProGluSerAspArgProAla 357
```

Db		
	121	GAAGATGAAGAAGATGATGTGTCAGAGGCTCTGAAGTGCCCAGAGTGACCGTC

Qy	358	GlyAlaGlnHisHisGlnLeuAsnGlyLysAsnGlyTyrGluArgGlyProGlnSerAlaLysGluA
Db	181	GGTGCCCAGCACCACCAGCTTAACGGCGAGCGGGAGGACCTCAGAGTGCCAAGGAGA

Qy	378	LysGluTrpThrProCysGlyTyrProHisGlnInGlyGlnAspGlyLysArgGlyProA
Db	241	AAGGAGTGGACCCCCTGCGGACCGGACCAGGGCCAGGATGAAGGGCGGGGCCAG

Qy	398	GlySerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyT
Db	301	GGCAGCGGCACCCGCCAGTGTTCTCCATGGCAGCCATGAACAACGAAGGGGGAA

Qy	418	SerValAlaThrGlyProAspSerProSerProValProLeuProProGlyLysP
Db	361	TCTKTTGCCACCGGGCCAGACTCCCGTCCCCCGTCCCTTTGCCCCAGGCAAAC

Qy	438	LeuProGlyAlaAspGlyThrProPheGlyCysProProGlyArgGlyLysGluLysP
Db	421	CTACCTGGGCGGCCGACACGGGACCCCCTTTGGCTGTCCTCCCGGCGCAAAGAGAAGC

Qy	458	AspProValGluTrpThrValMetAspValAlaGlyTyrPheThrGluAlaGlyP
Db	481	GATCCCGTCGAGTGGACCGTGATGGATGTCGTCGAATATTTTACTGAGGCTGGAT

Qy	478	GluGlnAlaThrAlaPheGlnGluGlnInGlnIleAspGlyLysSerLeuLeuLeuM
Db	541	GAGCAGGCGACAGTTTCCAAGAGCAGGAAATTGATGGCAAATCTTTGCTGCTCA

Qy	498	ArgThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleT
Db	601	CGCACAGATGTGCTCACCGGCCTGTCCATCCGCCTCGGGCCAGCCCTGAAAATCT

Qy	518	HisHisIleLysValLeuGlnGlyHisPheGluArgProSerProGlyLysP
Db	661	CACCACATCAAGGTGCTTCAGCAAGGCCACTTTGAGGATGATGACCCGATGGCT

Qy	538	Gly 538
Db	721	GGC 723

RESULT 7
AAH26490
ID   AAH26490 standard; cDNA; 1422 BP.
XX
AC   AAH26490;
XX
DT   12-NOV-2001 (first entry)
XX
DE   Rabbit low density lipoprotein binding protein 3 (LBP-3) cDNA.
XX
KW   Low density lipoprotein binding protein 3; LBP-3; LDL; rabbit;
KW   atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis;
KW   ss.
XX
OS   Oryctolagus cuniculus.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..955
FT   /*tag= a
FT   /partial
XX
PN   WO200164874-A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006356.
XX
PR   02-MAR-2000; 2000US-00517849.
PR   14-JUL-2000; 2000US-00616289.
XX

TON HEART FOUND INC.

ees RS,   Law SW,   Arjona AA;

65505/63.
82800.

d low density lipoprotein binding polypeptide for treating,
and/or identifying therapeutic agents for atherosclerosis.

Fig 13; 143pp; English.

sequence is that of cDNA encoding a portion (see AAB82800) of
t low density lipoprotein binding protein 3 (LBP-3). The cDNA
d following screening of a rabbit cDNA library for clones
Ps that bound to both native low density lipoprotein (LDL) and
A full-length sequence for rabbit LBP-3 cDNA is given in
he invention provides claimed polynucleotides encoding novel
s which are capable of binding to native and methylated LDL,
d polypeptides, termed LBPs, and biologically active fragments
es of them, as well as expression vectors, cells and methods
g the LBPs. Also claimed are methods of determining if an
t risk for atherosclerosis, methods for evaluating an agent
treating atherosclerosis, and methods for treating a cell
bnormality in structure or metabolism of LBP. Pharmaceutical
s comprising an LBP polypeptide or nucleic acid, and vaccine
s, are also claimed

22 BP; 265 A; 447 C; 442 G; 268 T; 0 U; 0 Other;

:   9.31e-25   Length: 1422
               1191.50   Matches: 223
ty: 95.24%   Conservative: 17
arity: 88.49%   Mismatches: 9
               41.81%   Indels: 3
               5   Gaps: 2

(1-538) x AAH26490 (1-1422)

```
rArgLeuGlyAlaLeuAlaLeuProArgArgGlyAspArgArgProGlyArgArgAlaProProAla 309
|||||||||||||||||:::|||||  |||||||||||||||||||||||||||||||||||||||||
CCGTCTCTGGAGCCGCTTGCGCTGCCCCCGCGGGGACAGGCCCGACGGGGCGCCACCGGCC      60

aSerAlaArgProSerArgSerLysArgGlyGlyGluGluArgValLeuGluLysGlu 329
||||||||     ||:::|||||  |||||||||||||||||||||||||||||||||||||
CAGCGCCCGCGCCGGAACAAGAGACTGGCAGGAGGAGCGAGTGCTTGAAAAAGAG    120

rGluGluAspAspAspGluAspGluGluGluAspGluAspAsp-----ValSerGluGly 347
|:::|||||||||||||||||||||||||||||||||||||||       |||||||||||
GGAGGAGGAGGAGGAGGAAGACGACGACGACGACGACGCGTCGTGTCCGAGGGC    180

rGluValProGluSerAspArgProAlaGlyAlaGlnHisHisGlnLeuAsn--Gly 366
||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
GGAGGTGCCCCAGAGACGATCGTCCCGCGGGTGCGCAGCATCACCAGCTGAATGGCCGC    240

rArgGlyProGlnSerAlaLysGluArgValLysGluTrpThrProCysGlyProHis 386
||||||||     |||||:::||||||   |||||||:::|||||   |||||||||||
GCGCGGCCCCAGAACCGCCAAGGAGCGGCCCAAGGAGTGGCCCGCGTGTGGCCCCCAC    300

rGlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThrArgGlnValPheSer 406
||||||:::||||||   |||||||||||   |||||||||||||||||||||||||||
GGGCCCAGGAGGAGGGCGGGGCCGCGGCCCGGCAGTGGCACCCGGCCAGGTGTTCTCC    360

rAlaAlaMetAsnLysGluGlyThrAlaSerValAlaThrGlyLeuProAspSerPro 426
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GCGGCCTTGAGTAACGAGGAGGGGGATCAGCCTCTTCGACCACCGGCCTGACTCCCCG    420

rProValProLeuProProGlyLysProLysAlaLeuProGlyAlaAspGlyThrProPhe 446
||||||||||||||||||||||||||||||||:::|||||||||||||||||||||||
CCCGGTGCCTTTGCCCCCGGAAGCCAGCCCCTCCCAGGAGCCCGATGGGACCCCCTTT    480

rCysProProGlyArgLysProSerAspProValGluTrpThrValMetAsp 466
```

one codes for novel human low density lipoprotein (LDL)
ein LBP-2 (see AAW49041). It was isolated by screening human
and foetal brain cDNA libraries with rabbit LBP-2 cDNA. cDNA
AAV32834-39) and encoded rabbit and human LBPs (see AAW49037-
ned. An abnormality in LBP metabolism or structure is
f a risk for atherosclerosis. The invention provides: methods
ing if an animal is at risk for atherosclerosis (e.g. for
eening); methods for treating atherosclerosis (including gene
ng e.g. LBP polypeptides to bind LDL and thereby prevent
atherosclerotic plaque; and methods for treating a cell
normality in LBP structure or metabolism. Pharmaceutical and
ositions are also provided, as well as recombinant vectors
is used to produce recombinant LBP

8 BP; 252 A; 368 C; 321 G; 266 T; 0 U; 1 Other;

	3.21e-24	Length:	1208
	1170.00	Matches:	217
y:	100.00%	Conservative:	0
rity:	100.00%	Mismatches:	0
	41.05%	Indels:	0
		Gaps:	2

(1-538) x AAV32838 (1-1208)

GluArgValLeuGluLysGluGluGluAspAspAspGluAspGluGlu 341
|||||||||||||||||||||||||||||||||||||||||||||||
GAGGCGAGTACTTGAGAAGAAGAGGAGGAAGAAGATGATGAAGATGAAGAA 60

AspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHis 361
|||||||||||||||||||||||||||||||||||||||||||||||||||||||
GATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCCGCAGGTGCCCAGCAC 120

GlnLeuAsnGlyGluArgGlyProGlnSerAlaAlaLysGluArgValLysGluTrpThr 381
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CAGCTTAACGGCGAGCGCGGGACCTCAGAGTGCCCAAGGAGAGGGTCAAGGAGTGGACC 180

CysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThr 401
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TGCGGACCGCACCAGGGCCAGGATGAAGGGCGGGGGCCAGCCCCGGGCAGCGGCACC 240

GlnValPheSerMetAlaAlaMetAsnLysGluGlyValGlyThrAlaSerValAlaThr 421
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGAACAGCTTCTGTTGCCACC 300

ProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAla 441
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CCAGACTCCCCGTCCCCCGTGCCTTTGCCCCCAGGCAAACCAGCCCTACCTGGGGCC 360

GlyThrProPheGlyCysProProGlyArgLysGluLysProSerAspProValGlu 461
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GGGACCCCCTTTGGCTGTCCTCCCGGGCGCAAAGAGAAGCCATCTGATCCCGTCGAG 420

ThrValMetAspValValGluTyrPheThrGlyAlaGlyPheProGluGlnAlaThr 481
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ACCGTGATGGATGTCGTCGAATATTTTACTGGAGGCTGGATTCCGGAGCAGGCGGACA 480

PheGlnGluGlnIleIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspVal 501
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TTCCAAGAGCAGGAAATTGATGGCAAATCTTTGCTGCTCATGCAGCGCACAGATGTG 540

ThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisLeuLys 521
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ACCGGCCTGTCCATCCGCCTCGGGCCAGCCCTGAAAATCTACGAGCACCACATCAAG 600

LeuGlnGlnGlyHisProPheGluAspAspAspProAlaProAspGlyPheLeuGly 538
|||||||||||||||||||||||||||||||||||||||||||
CCTTCAGCAAGGCCACTTTGAGGATGATGACCCCGATGGCTTCTTAGGC 651

ndard; cDNA; 1208 BP.

Alignment Scores:

Pred. No.:	3.21e-24	Length:	1208
Score:	1170.00	Matches:	217
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	41.05%	Indels:	0
DB:		Gaps:	0

US-09-976-740-43 (1-538) x AAH26494 (1-1208)

Qy   322 GluGluArgValLeuGluLysGluGluGluAspAspAspGluAspGluu
         ||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GAAGAGCGAGTACTTGAGAAGAAGAGGAGGAAGAAGATGATGAAGATGAAGATG

Qy   342 AspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaG
         ||||||||||||||||||||||||||||||||||||||||||||||||||||

DR   P-PSDB; AAB82799.
XX
PT   New isolated low density lipoprotein binding polypeptide for tr
PT   diagnosing and/or identifying therapeutic agents for atheroscle
XX
PS   Example 2; Fig 12; 143pp; English.
XX
CC   The present sequence is that of cDNA encoding a portion (see Al
CC   novel rabbit low density lipoprotein binding protein 2 (LBP-2).
CC   was isolated following screening of a rabbit cDNA library for c
CC   encoding LBPs that bound to both native low density lipoprotein
CC   methyl LDL. A full-length sequence for LBP-2 is given in AAH265
CC   invention provides claimed polynucleotides encoding novel polyp
CC   which are capable of binding to native and methylated LDL, the
CC   polypeptides, termed LBPs, and biologically active fragments ar
CC   analogues of them, as well as expression vectors, cells and met
CC   producing the LBPs. Also claimed are methods of determining if
CC   is at risk for atherosclerosis, methods for evaluating an agent
CC   in treating atherosclerosis, and methods for treating a cell ha
CC   abnormality in structure or metabolism of LBP. Pharmaceutical
CC   compositions comprising an LBP polypeptide or nucleic acid, and
CC   compositions, are also claimed
XX
SQ   Sequence 1362 BP; 259 A; 421 C; 419 G; 263 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:   6.12e-22   Length: 1362
Score: 1086.50   Matches: 203
Percent Similarity: 94.83%   Conservative: 17
Best Local Similarity: 87.50%   Mismatches: 9
Query Match: 38.12%   Indels: 3
DB: Gaps: 2

US-09-976-740-43 (1-538) x AAH26489 (1-1362)

Qy   310 AlaSerAlaArgProSerArgSerArgGlyGlyGluArgValLeuGlu
             :::||| ::|||||
Db   1 GCCAGCGCCCGCCGCGCGCGCAACAAGAGACTGCGCGAGGAGCGAGTGCTTGAA

Qy   330 GluGluGluAspAspAspGluGluArgGluGluAspAsp-----ValSer
           ||||||||||| |||::::::::|||||||:::::: |||
Db   61 GAGGAGGAGGAGGAGGACGACGAGGAGGAAGACGACGACGTCGTGTCC

Qy   348 SerGluValProGluSerAspArgProAlaGlyAlaGlyGlnHisHisGlnLeuAsn
Db   121 TCGGAGGTGCCCGAGAGCGATCGTCCCGCGGGTGCGCAGCATCACCAGCTGAAT

Qy   367 GluArgGlyProGlnSerAlaLysGluArgValLysGluArgTrpProCysGly
             :::: |||||||||| :::|||
Db   181 GAGCGCGGCCGCAGACCCCAGAGCGCCAAGGAGTGGTGCTGTGTGGGC

Qy   387 GlnGlyGlnAspGluGlyArgGlyArgProAlaProGlySerGlyThrArgGlnVal
             :::|| |||||||
Db   241 CCTGGCCAGGAGGAAGGGGGGGGGCCGGCCGCCGGGGCAGTGGCACCCGCCAGGTG

Qy   407 MetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThrGlyProAsp
Db   301 ATGGCGGCCTTGAGTAAGGAGGGGGGATCAGCCTCTTCGACCACCGGGCCTGAC

Qy   427 SerProValProLeuProProGlyLysProAlaLeuProGlyAlaAspGlyThr
Db   361 TCCCCGGTGCCTTTGCCCCCGGGAAGCCAGCCCTCCCAGGAGCCGGATGGGACC(

Qy   447 GlyCysProProGlyArgLysProSerAspProValGluTrpThrVal
Db   421 GGCTGCCCTGCCCGGCGCAAAGAAGACCCGGCAGACCCCGTGGAGTGGACAGTC

Qy   467 ValValGluTyrPheThrGluAlaGlyProGluGlnAlaThrAlaPheGln(
Db   481 GTCGTGGAGTACTTCACCGAGGCGGGCCTTCCCTGAGCAAGCCACCACGCTTTCAG(

Qy   487 GluIleAspGlyLysSerLeuLeuMetGlnArgThrArgValLeuThrHisGly?

TGATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCTCGCAGGTGCCCAGCAC 120

aGlnLeuAsnGlyGluArgGlyGlnSerAlaLysGluArgValLysGluArgTrpThr 381
CCAGCTTAACGGCGAGCGGGACCTCAGAGTGCCAAGGAGGAGGGTCAAGGAGTGGACC 180

bCysGlyProHisGlnGlyGlnAspGlyGlyArgGlyProAlaProGlySerGlyThr 401
CTGCGGACCGCACCAGGCCAGGATGAGGGCGGGGGCCCAGCCCCGGGCAGCGGCACC 240

gGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyGlyThrAlaSerValAlaThr 421
CCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGAACAGCTTCTGTTGCCACC 300

yProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAla 441
GCCAGACTCCCCGTCCCCGTGCCTTTGCCCCCAGGCAAACCAGCCCTACCTGGGGCC 360

pGlyThrProPheGlyCysProProGlyArgLysProSerAspProValGlu 461
CGGGACCCCCTTTGGCTGCCTCCCCGGGCGCAAAGAAGCCATCTGATCCCGTCGAG 420

oThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThr 481
GACCGTGATGATGTCGTCGAATATTTTACTGAGGCTGGATTCCCCGAGCAGGCGACA 480

aPheGlnGluGlnGluLeuAspGlyLysSerLeuLeuMetGlnArgThrArgAspVal 501
CTTTCCAAGAGCAGGAAATTGATGGCAAATCTTTGCTCTCATGCAGCGCCACAGATGTG 540

iThrGlyLeuSerIleArgLeuGlyLeuGlyProAlaLeuLysIleTyrGluHisHisIleLys 521
CACCGGCCTGTCCATCCGCCTCGGGCCCGCCAGCCCTGAAAATCTACGAGCACCATCAAG 600

LLeuGlnGlnGlyHisPheGluGlnAspAspAspAspProAspProGlyPheLeuGlu 538
GCTTCAGCAAGGCCACTTTGAGGATGATGACCCCGATGGCCTTCTTAGGC 651

indard; cDNA; 1362 BP.

(first entry)

lensity lipoprotein binding protein 2 (LBP-2) cDNA.

lipoprotein binding protein 2; LBP-2; LDL; rabbit;
osis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;

cuniculus.

Location/Qualifiers
   1..955
   /*tag= a
   /partial

A2.

: 2001WO-US006356.
: 2000US-00517849.
: 2000US-00616289.

ON HEART FOUND INC.

ees RS, Law SW, Arjona AA;

5505/63.

SQ   Sequence 1134 BP; 248 A; 294 C; 366 G; 225 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.:   Length: 1134
Score: 1.46e-14   811.00   Matches: 151
Percent Similarity: 100.00%   Conservative: 1
Best Local Similarity: 99.34%   Mismatches: 0
Query Match: 28.46%   Indels: 0
DB: 3   Gaps: 0

US-09-976-740-43 (1-538) x AAC59574 (1-1134)

```
Qy   387 GlnGlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThrArgGlnValP
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   921 CAGGGCCAGGATGAGGAGGGCGGGGGCGGCCAGCCCGGGCAGCGGCACCCGCCAGGTGT

Qy   407 MetAlaAlaMetAsnLysGlyGluGlyGlyThrAlaSerValAlaThrGlyProAspS
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   861 ATGGCAGCCATGAACAAGGAACAGGGGAACAGCTTCTGTTGCCACCGGGCCAGACT

Qy   427 SerProValProLeuProProGlyLysProAlaLeuProGlyAlaAspGlyThrP
         |||||||||||||||||||||||||||||||||||||||:::|
Db   801 TCCCCCGTGCCTTTGCCCCCAGGCAAACCAGCCCTTACCTGGGGCCGACGGGTCCC

Qy   447 GlyCysProProGlyArgLysGluLysProSerAspProValGluTrpThrValM
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   741 GGCTGTCCTCCCGGGCGCAAAGAGAAGCCATGGACATCCGGATCCCGTCGAGTGGACCGTGA

Qy   467 ValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThrAlaPheGlnG
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   681 GTCGTCGAATATTTTACTGAGGCTGGATTCCCGGAGCAGGCAGCAGCTTTCCAAG

Qy   487 GluIleAspGlyLysSerLeuLeuMetGlnArgThrAspValLeuThrGlyL
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   621 GAAATTGATGGCAAATCTTTGCTGCTCATGCAGCGCACAGATGTGCTCACCGGCC

Qy   507 IleArgLeuGlyProAlaLeuLysIleTyrGluHisIleLysValLeuGlnG
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   561 ATCCGCCTCGGCCCAGCCCTGAAAATCTACGAACACCATCAAGGTGCTCAGC

Qy   527 HisPheGluAspAspProAspGlyPheLeuGly 538
         ||||||||||||||||||||||||||||||||||
Db   501 CACTTTGAGGATGATGACCCCGATGGCTTCTTAGGC 466
```

RESULT 12
ADB49888/c
ID   ADB49888 standard; DNA; 460 BP.
XX
AC   ADB49888;
XX
DT   04-DEC-2003 (first entry)
XX
DE   Primary rat hepatocyte toxicity modelling related gene SEQ ID NO
XX
KW   toxic effect; gene expression profile; hepatotoxicity; diagnosti
KW   toxicity marker; toxicity progression; drug screening;
KW   primary rat hepatocyte toxicity modelling; gene; ds.
XX
OS   Rattus norvegicus.
XX
PN   WO200306599-A2.
XX
PD   14-AUG-2003.
XX
PF   04-FEB-2003; 2003WO-US003482.
XX
PR   04-FEB-2002; 2002US-0353171P.
PR   13-MAR-2002; 2002US-0363534P.
PR   08-APR-2002; 2002US-0370248P.
PR   10-APR-2002; 2002US-0371134P.
PR   10-APR-2002; 2002US-0371135P.
PR   10-APR-2002; 2002US-0371150P.
PR   11-APR-2002; 2002US-0371413P.

```
Db  ...TCGACGGCAAGTCCCTGCTCTCATGCAGCGCACCGATGTCCTCACCGGCCTGTCC 600

Qy  ...ArgLeuGlyProAlaLeuLysIleTyrGluHisIleLysValLeuGlnGlnGly 526
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  ...CGCCTGGGCCCAGCCGTTGAAAATCATGAGCACCATATCAAGGTGCTGAGCAGGGT 660

Qy  ...PheGluAspAspProAspGlyPheLeuGly 538
        |||||||||||||||||||||:::::|||||
Db  ...CTCGAGGACGATGACCCGGAAGGCTTCCTGGGA 696
```

RE
AA
ID ...dard; cDNA; 1134 BP.
XX
AC
DT (first entry)
XX
DE ...d protein gene 9 SEQ ID NO:19.
XX
KW ...ed protein; diagnosis; neuroprotective; cytostatic;
KW ...immunomodulatory; muscular active general; vulnerary;
KW ...nal; nephrotropic; antiinfective; gynaecological;
KW ...arial; gene therapy; detection; cancer; chromosome marker;
KW ...lentification; neural disorder; immune disorder;
KW ...order; reproductive disorder; gastrointestinal disorder;
KW ...sorder; cardiovascular disorder; renal disorder;
KW ...a disorder; wound healing; infectious disease; preservative;
KZ ...e; 88.
XX
PN ...A1.
XX
PD ...2000WO-US006822.
XX
PR ...99US-0126054P.
PR ...99US-0169916P.
XX
FA ...N GENOME SCI INC.
PA
FI ...ben SM, Komatsoulis G;
PT
    ...7666/55.
    ...1307.
XX
CC ...ed proteins and gene sequences encoding them, useful for
CC ...eventing, and treating disorders such as cancer,
CC ...disorders and immune system disorders.
XX
    ...a 344; 429pp; English.

CC ...eotide sequences given in AAC59566 to AAC59614 encode the
CC ...ed proteins given in AAB34299 to AAB34347. AAB34348 to
CC ...resent human secreted polypeptide sequences and proteins
CC ...o them, which are given in the exemplification of the present
CC ...man secreted proteins have activities based on the tissues
CC ...e genes are expressed in. Example of activities include:
CC ...ive; cytostatic; cardioactive; immunomodulatory; muscular
CC ...al; vulnerary; gastrointestinal; nephrotropic; antiinfective;
CC ...al; and antibacterial. The polynucleotides can be used for
CC ...of various disorders such as cancer, chromosome
CC ...on, as chromosome markers, and for numerous other diagnostic
CC ...purposes. The secreted proteins can be used to treat
CC ...ch as neural, immune, muscular, reproductive,
CC ...inal, pulmonary, cardiovascular, renal, and proliferative
CC ...ound healing, and infectious diseases. The proteins can also
CC ...food additive or preservative to increase or decrease
CC ...bilities. AAC59557 to AAC59565 and AAB34298 represent
CC ...ed in the exemplification of the present invention

; 2002US-0373601P.
; 2002US-0373602P.
; 2002US-0374139P.
; 2002US-0378370P.
; 2002US-0378652P.
; 2002US-0378653P.
; 2002US-0378665P.
; 2002US-0394230P.
; 2002US-0394253P.
; 2002US-0407688P.
; 2003US-0442900P.

E LOGIC INC.

Porter M, Johnson K, Higgs B, Castle A, Orr M;

31472/69.

if a compound induces a toxic effect on a tissue or cell, for
hepatotoxic compounds, comprises comparing a gene expression
a tissue or cell sample to a database of Tox mean and non-Tox

EQ ID NO 430; 874pp; English.

invention describes a method for determining whether a
duces a toxic effect on a tissue or cell. The method comprises
gene expression profile of a tissue or cell sample exposed to
d, and comparing the gene expression profile to a database
data or information on the Tox mean and non-Tox mean value.
is useful for predicting or identifying at least one toxic
ticularly hepatotoxicity, of a test or unknown compound. The
d in the specification are useful as diagnostic or toxicity
the prediction or identification of the physiological state
r cell sample that has been exposed to a compound, or to
predict the toxic effects of a compound or an agent. These
used as markers for monitoring toxicity progression or for
ing. The present sequence represents a primary rat hepatocyte
delling related gene sequence from the present invention.

0 BP; 110 A; 119 C; 126 G; 105 T; 0 U; 0 Other;

:

ty:	4.27e-05	Length:	460
arity:	451.00	Matches:	82
	82.52%	Conservative:	3
	79.61%	Mismatches:	12
	15.82%	Indels:	6
	9	Gaps:	1

(1-538) x ADB49888 (1-460)

uTrpThrProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGly 398
    |||:|:|||||||||||||||||||||||||||||||||||||||||||
STGGTCGCCCTGTGGACCTTTCCAGGGCCCAGGATGAGAGGGCGGGGGACCAGCACCTGGC 400

rGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGlyGlyThrAlaSer 418
    :|||||||||||||||||||||||||||||||:|||
CTGCACACACCAGGTGTTCTCGATGACAGCTATGAATAAAGAAAGGGGATCGGCTTGT 340

lAlaThrGlyProAspSerProSerProValProLeuProProGlyLysProAlaLeu 438
    |||||||||||||||||||||||||||||||||||||||||||||||||
TACAGCTGTCTCCAGATTCTCCATCTCCGTGCCTTTGCCTCCAGGAAAACCAGCCCTA 280

oGlyAlaAspGlyThrProPheGlyCysProProGlyArgLysGluLysProSerAsp 458
    ||||||||||||||||||||||||||||||||||::::|||
TGGGGCTGATGGGACACCATTTGGCTGTCCTCCTCGGCGCAAGGAGAAGCCAACGGAC 220

oValGluTrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGlu 478
    ||||||||||||||||||||||||||||----SerSerSer
AGTGGAGTGGACAGTCATGGATGTGGTT-------------TTTCCTCGT 178

Qy   479 GlnAlaThr 481
                |||
Db   177 CCCACCACC 169

RESULT 13
AAI99682_39/c
Continuation (40 of 45) of AAI99682 from base 3900001 (Mycobacteriu
WP Sequence split into 45 fragments LOCUS AAI99682 Accession Aai99
WP Fragment Name   Begin   End
WP AAI99682_00   1   110000
WP AAI99682_01   100001   210000
WP AAI99682_02   200001   310000
WP AAI99682_03   300001   410000
WP AAI99682_04   400001   510000
WP AAI99682_05   500001   610000
WP AAI99682_06   600001   710000
WP AAI99682_07   700001   810000
WP AAI99682_08   800001   910000
WP AAI99682_09   900001   1010000
WP AAI99682_10   1000001   1110000
WP AAI99682_11   1100001   1210000
WP AAI99682_12   1200001   1310000
WP AAI99682_13   1300001   1410000
WP AAI99682_14   1400001   1510000
WP AAI99682_15   1500001   1610000
WP AAI99682_16   1600001   1710000
WP AAI99682_17   1700001   1810000
WP AAI99682_18   1800001   1910000
WP AAI99682_19   1900001   2010000
WP AAI99682_20   2000001   2110000
WP AAI99682_21   2100001   2210000
WP AAI99682_22   2200001   2310000
WP AAI99682_23   2300001   2410000
WP AAI99682_24   2400001   2510000
WP AAI99682_25   2500001   2610000
WP AAI99682_26   2600001   2710000
WP AAI99682_27   2700001   2810000
WP AAI99682_28   2800001   2910000
WP AAI99682_29   2900001   3010000
WP AAI99682_30   3000001   3110000
WP AAI99682_31   3100001   3210000
WP AAI99682_32   3200001   3310000
WP AAI99682_33   3300001   3410000
WP AAI99682_34   3400001   3510000
WP AAI99682_35   3500001   3610000
WP AAI99682_36   3600001   3710000
WP AAI99682_37   3700001   3810000
WP AAI99682_38   3800001   3910000
WP AAI99682_39   3900001   4010000
WP AAI99682_40   4000001   4110000
WP AAI99682_41   4100001   4210000
WP AAI99682_42   4200001   4310000
WP AAI99682_43   4300001   4410000
WP AAI99682_44   4400001   4411529

Alignment Scores:
Pred. No.:   0.00927   Length: 110000
Score: 417.00   Matches: 193
Percent Similarity: 34.89%   Conservative: 31
Best Local Similarity: 30.06%   Mismatches: 199
Query Match: 14.63%   Indels: 223
DB: 4   Gaps: 32

US-09-976-740-43 (1-538) x AAI99682_39 (1-110000)

Qy   4 ProProAlaLeuPro---ProProGluThrAlaAlaAlaAlaThrAlaAla
          |||||||||||| |||||||||| |||||||||
Db 33207 CCGCCTGCACCGCCAGCGCCGCCGGAGCC-GTTGGTGCCCACCACCGCTGTT

Qy   23 --------------------------------------SerSerSer
                                                 |:|::
Db 33148 CGCTCCGCCTTCTCCGCCGGCGCCGCCGGCGAACCGCGCGCCACCGGTAGGCGCT

```
Qy   ProHisTyrGlnTrpIleLeuAspThrIleAspSerLeuArgSerArgLysAla  47
          ::: |||    |||::: |||
Db   GGCCGCAGCCGCCACCTGCCACCACCAGCACCACCCGTAC-CGCCGGTAC  33030

Qy   ProAspLeu-----------GluArgIleCysArgMetValArgArg  60
     |||   |||
Db   CGATCCCGGCGTTACCGACGCTGCCCACCGCCGGTGCCCGCCGTACCGATGG  32970

Qy   HisGlyProGlu-------------------  65
     |||   |||
Db   CACCCGGCCCCGCCGGCTCCGCCGGTCGCCGGTGCCCGGCCGGCCGC  32910

Qy   -----------------ProGluArgThrArgAlaGluLeuGluLys  75
                      :::||| |||    |||   :::
Db   TGCCGGTGGGGTTATCGCCGGCCCCCAGCGGCCCGGCCTTGTCCGC  32850

Qy   IleGlnGlnArgAlaValLeuArgValSerTyrIleSerGlyTyrArgAsn  95
     :::|||                              :::
Db   TGCCGGCAGCGCCACCAGACCGTTGGTGCCCGGCACCGC---TGCTACCGCCCT  32793

Qy   AlaArgValGlnProProArgArgGlyAlaThrProProProArgAlaPro  115
        |||    |||       |||||||
Db   CGCCGG-----CCCCGCCGCGCCG-CCTTTCCCGCCGGTGCCGCCGGTGCCGCCG  32740

Qy   ------------GlyAlaProAlaAlaAlaAlaAlaAlaAlaPro-------  127
                 |||    ||||||
Db   CCGGTGGGGTTGTCGGCGCCGACACCGCCAGCACCACCCGGGGCCGCCGCCGCCG  32680

Qy   -------------ProProThr--------ProAlaPro  133
                  |||      |||||||
Db   CCGCCTTGCCCGCCGGAGCCGTTGGTGCGCCCAACCCCGGTGTTGCCCGGCCCCG  32620

Qy   ProProProAlaProValAlaAlaAlaAlaProAlaArgAlaArgAlaAlaAla  153
     |||||||
Db   CCCCCGCCGGCTCCACCGGAAAACCCGTGCCCGGTGGCACCGGTAGCCGTCGCA  32560

Qy   -----AlaAlaThrAlaProProSerPro------GlyProAlaGlnProGlyPro  169
          |||||:::||| |||
Db   GTGCCGGCGTCGCCGCCGCCGCCTTGGCCGCCGGTGCCGCCGGATACCG  32500

Qy   AlaGlnArgAlaAlaAlaProLeuAlaAlaPro---ProProAlaProAlaProPro  188
     |||||       ||||||
Db   GCCTTGCCGCCGCGGCGACAACCCCGCGGTTCCTCCGGTGCCGGGCCCCCG  32443

Qy   ----------ValAlaProAlaGlyProArgArgAlaProAlaProPro  201
               |||||||
Db   CGCCCGGCGCCGGTACCGCCAGTCCACCCGCGCGCCGTCGGGCCCAATCCCG  32383

Qy   AlaValAlaAlaArgGluProProLeuProPro---------ProProGlnPro  217
     |||:::|||   |||||:||
Db   GCATTATCAGACACCGGAGCCACCCATGCCGGCGCGCCGCCTTGGCCGGTGCCG  32323

Qy   AlaProProGlnGlnGlnGlnProPro----------ProProGln  230
     ||||||
Db   GCACCACCGGAGCCGTTGATGCCGGCAATGGCGTTGCCGCCCGCACG  32263

Qy   GlnProProGlu----------GlyGlyAlaVal  240
     ||||||
Db   CCGGGCCCCGCCAGC-GAACCCGTACCACCGGTTAGACCGTGCTGGCGGGGGCGTC  32204

Qy   AlaGly---------------GlyAlaAlaArgProVal  249
     ||||||
Db   GCCGGCGCCTCCGGCACCGCCAGCCCACCCTGCCCGCCGGTTGCCGCCAACCCCAAC  32144

Qy   LeuArg-----------GluValValArgTyrLeuGlyGly----------  260
     ||||||
Db   ACCCGCGCGGCCTCCGGCGCTGAAGAGCTGGCCCCGGCACCACCGGCCCCGCCGAG  32084

Qy   -----------------  260
Db   AGCCACCGCGCGACACCCCTTACCACCAGTCCACCGACACCCCCAGAACGCC  32024

Qy   ---SerGlyGlyAlaGlyGlyArgLeuThrArgGlyValArgGlnGlyLeuLeu---  277
```

Right column:

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Db   32023  ATCTCGCCGCCGCCGTGCCGCCTTGCCGCCGAGGCGCCC
                               |||||        |||::: :::
Qy   278    --------GluGluAlaAlaAla
Db   31963  GCCAGCGCCGCCAGCAGTGCCGCGACCGCCGCCGCCGCCGGTA
                ::::::::: ||||||
Qy   284    ------ArgGlyArgLeuArgThrArgLeuGlyAla--------LeuA
Db   31903  CGTCCCGCCGTACCACCCAACGCGCCACCATGCGTCCGGCACCACCTGCCCCG
Qy   298    ProArgGlyAspArg--ProGlyArgAlaProAlaAlaSerAlaArgProS
                |||          ::||| |||:::
Db   31843  CCCGCGGCCCGCCGCCCCGCCGGTGCCCAGCCATCCGCCGTGCCGCCGACT
Qy   317    SerLysArgGlyGlyGluGluArgValLeuGluLysGluGluGluAspAspA
Db   31783  GTGTCCGCCGT-------
                |||
Qy   337    AspGluAspGluGluAspAspValSerGluGlySerGluValPro------
Db   31771  ------------------------CCCGCCGGTAGCACCGGGCCCGCCGTCGGTG
                                        |||||||
Qy   353    SerAspArgProAlaGlyAlaGlnHisHisGlnLeuLeuAsnGlyGluArgGlyTyrProG
                |||||||:::
Db   31735  CCCACCGCACCGCCGGCGCCGAA--CAGCAGCTCGGCGCGCCGGGCCGGCCGGCCCCG
Qy   373    AlaLysGluArgValLysGluThrProCysGlyProHisGlnGlyGlnAspG
                                            :::       |||||
Db   31678  GCCGCCACCGGCCCCCACCGAC---ACCGCCGGCCCCGCCGCCCCAGATC
Qy   393    ArgGlyProAla------ProGlySerGlyThrArgGlnValPheSerMetAlaA
                |||                |||          |:||
Db   31624  ACCGGGCCCGCCGCCCGCCGCCGGTGCCCGCCACCGGCCCCCACCGACCGCCGGCCG
Qy   411    AsnLysGlu--------------GlyGlyThrAlaSerValAlaThrGly-
                |||                   ||||||
Db   31564  AACCCCGACAAGCACCACCACCGCCCCGGCACCGGTGCCCCCACCGCTC
Qy   424    pSerProSerProValProLeu--------ProProGlyLysPro
                :::|||                      |||||
Db   31504  GGCCCCGCCGGCGCCGTTGCCCCCACAATCCGGCGGGCCCAGGCCCCGGCCG
Qy   438    uProGlyAlaAspGlyThrProPheGlyCysProGlyArgGlyLysGluLysProG
                |||                                :::|||
Db   31444  GCCGGGCGCGCCCCGGCTGCCCCG-----GCCCCGCCGTTGCCGAACAGCAGACCG
Qy   458    pPro  459
          |||
Db   31390  CCCG  31387
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RESULT 15

ABQ49732/c
ID   ABQ49732/c standard; DNA; 533 BP.
XX
AC   ABQ49732;
XX
DT   12-JUL-2002 (first entry)
XX
DE   Oligonucleotide for detecting cytosine methylation SEQ ID NO 3(
XX
KW   Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagr
KW   drug; side effect; cancer; central nervous system; cardiovascul
KW   gastrointestinal; respiratory system; single nucleotide polymor
KW   SNP; cell differentiation; ds.
XX
OS   Homo sapiens.
XX
PN   WO200218632-A2.
XX
PD   07-MAR-2002.
XX
PF   01-SEP-2001; 2001WO-EP010074.
XX
PR   01-SEP-2000; 2000DE-01043826.
PR   05-SEP-2000; 2000DE-01044543.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
DR   WPI; 2002-371829/40.
XX
PT   Determining the degree of cytosine methylation in genomic DNA,
PT   diagnosis and prognosis, comprises selective hybridization of a
PT   from chemically treated DNA.
XX
PS   Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC   This invention describes a novel method for determining the deg
CC   methylation of a particular cytosine in a motif 5'-CpG-3', pres
CC   genomic sample of DNA. The sample is treated chemically to conv
CC   cytosine (C) but not methylated C, to uracil, then part of the
CC   DNA that contains the target C is amplified to form a labeled a
CC   The amplicon is hybridised to two classes, each with at least o
CC   of oligonucleotide and/or peptide-nucleic acid (PNA) oligomers
CC   degree of hybridisation to both classes is determined from the
CC   the amplicon. From the ratio of labels hybridised to the two cl
CC   oligomers, the degree of methylation is calculated. The method
CC   (i) for diagnosis and/or prognosis of side effects of therapeut
CC   and of a wide range of diseases, e.g. cancer, disorders of the
CC   nervous, cardiovascular, gastrointestinal and respiratory syste
CC   particularly by detecting mutations or single nucleotide polymo
CC   (SNP's); and (ii) for differentiation of cell or tissue types a
CC   investigating cell differentiation. The method allows the methy
CC   status of many C residues to be determined simultaneously. ABQ1
CC   ABQ54121 represent genomic DNA sequences used to illustrate the
CC   for determining the degree of cytosine methylation described in
CC   disclosure of the invention
XX
SQ   Sequence 533 BP; 55 A; 75 C; 187 G; 216 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:   0.000435   Length: 533
Score: 415.00   Matches: 82
Percent Similarity: 85.45%   Conservative: 12
Best Local Similarity: 74.55%   Mismatches: 15
Query Match: 14.56%   Indels: 1
DB: Gaps: 0

US-09-976-740-43 (1-538) x ABQ49732 (1-533)

Qy   4 ProProAlaLeuProProProGluThrAlaAlaAlaAlaThrThrAlaAlaAlaAla

```
CCGACCCTACCCCGCCGAAAAACGACGACGACCGCCACCACGACGACGACCGCGCCCTCG 343

SerAlaAlaSerProHisTyrGlnGluTrpIleLeuAspThrIleAspSerLeuArg  43
|||||||||||||||||||||||:::  |||||:|:::||||||||||||||||||
TCCGGCCGCTTCCCCGACTACCACCAAAAATAAATCCTAAACACCATCGACTCGCTACGC 283

ArgLysAlaArgProAspLeuGluArgIleCysArgMetValArgArgArgHisGly  63
||||||  |||||||::::||||| |||:::::||||||||||||||||
CGCAAAAACGGCACCGAACCTAAAACGCATCTACCGAATAATACGACGACGACACGAC 223

GluProGluArgThrArgAlaGluLeuGluLysGlnIleGlnArgAlaValLeu  83
::::|||:::||||||||||||||||||||||||||||||||||||||||
AAACCGAAAACGCACGCGCCGCCGAACTCGAAAAACTAATCCAACAACCGCCGTACTC 163

ValSerTyrLysGlySerIleSerTyrArgAsnAlaAlaArgValGlnProProArg 103
:::::||||||  :::|||||||||||||||  |||||||||||||
ATCAACTACACAAAAAAACATCTCGTACCCGCAACGCCGACGCGCGTCCAACCGCCCCGA 103

GlyAlaThrPro-ProAlaProPro 112
||||| |||  ||||||
GAAACCACCCCCGTCCGAATCCACCG  75
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March 12, 2004, 21:10:03
6 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

leic search, using frame_plus_p2n model

March 12, 2004, 20:05:17 ; Search time 182.406 Seconds
(without alignments)
1636.805 Million cell updates/sec

US-09-976-740-43
2850
1 MAGPPALPPPETAAAATTAA.........HIKVLQQGHFEDDDDPDGFLG 538

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

682709 segs, 277475446 residues

hits satisfying chosen parameters: 1365418

ength: 0
ength: 2000000000

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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spool_p/US09976740/runat_10032004_094549_19564/app_query.fasta_1.1898
ts_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCI=0
S=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
GN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
FMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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UERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 - FGAPOP=6
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Issued Patents_NA:*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

is the number of results predicted by chance to have a
ter than or equal to the score of the result being printed,
ived by analysis of the total score distribution.

SUMMARIES

Query Match	Length	DB	ID	Description
100.0	1614	4	US-09-616-289-45	Sequence 45, Appl
91.8	12425	4	US-09-616-289-50	Sequence 50, Appl
91.0	2561	4	US-09-616-289-48	Sequence 48, Appl
51.1	1617	4	US-08-979-608A-11	Sequence 11, Appl
51.1	1617	4	US-09-517-849-11	Sequence 11, Appl
51.1	1617	4	US-09-616-289-11	Sequence 11, Appl
41.8	1422	4	US-08-979-608A-13	Sequence 13, Appl
41.8	1422	4	US-09-517-849-13	Sequence 13, Appl
41.8	1422	4	US-09-616-289-13	Sequence 13, Appl
41.1	1208	4	US-08-979-608A-16	Sequence 16, Appl
41.1	1208	4	US-09-517-849-16	Sequence 16, Appl
41.1	1208	4	US-09-616-289-16	Sequence 16, Appl

						ID	
13		1086.5	38.1	1362	4	US-08-979-608A-12	Sequence
14		1086.5	38.1	1362	4	US-09-517-849-12	Sequence
15		1086.5	38.1	1362	4	US-09-616-289-12	Sequence
16	c	417	14.6	4411529	3	US-09-103-840A-1	Sequen
17	c	411.5	14.4	4403765	3	US-09-103-840A-2	Sequen
18		394.5	13.8	4403765	3	US-09-103-840A-2	Sequen
19		394.5	13.8	4411529	3	US-09-103-840A-1	Sequen
20	c	391	13.7	2214	3	US-08-864-038A-1	Sequen
21	c	391	13.7	3331	3	US-08-864-038A-2	Sequen
22	c	391	13.7	3331	3	US-08-864-038A-4	Sequen
23		390	13.7	425	1	US-09-621-976-9791	Sequen
24	c	389	13.6	8438	1	US-07-945-283-1	Sequen
25	c	386	13.5	1926	4	US-09-249-585A-2	Sequen
26	c	386	13.5	1926	4	US-09-410-399-3	Sequen
27		386	13.5	2580	4	US-09-050-863-2	Sequen
28	c	386	13.5	2580	4	US-09-359-081-2	Sequen
29		386	13.5	5452	2	US-09-130-114-1	Sequen
30		386	13.5	8705	4	US-09-647-344A-14	Sequen
31	c	386	13.5	9600	3	US-08-910-647-1	Sequen
32		386	13.5	9600	4	US-09-620-925-1	Sequen
33		386	13.5	10596	1	US-07-884-811-15	Sequen
34	c	386	13.5	10596	1	US-07-885-971-15	Sequen
35	c	386	13.5	10596	1	US-08-087-783A-15	Sequen
36	c	386	13.5	10596	1	US-08-194-088B-15	Sequen
37		386	13.5	10596	2	US-08-194-087-15	Sequen
38	c	386	13.5	10596	5	PCT-US93-04648-15	Sequen
39		386	13.5	16080	4	US-09-724-566A-48	Sequen
40		372.5	13.1	2481	4	US-09-894-998A-35	Sequen
41	c	360	12.6	2793	1	US-08-209-747-1	Sequen
42	c	360	12.6	2793	1	US-08-458-298-1	Sequen
43	c	357	12.5	71989	4	US-09-443-501A-2	Sequen
44		352	12.4	33529	3	US-09-144-085-3	Sequen
45	c	351.5	12.3	12001	1	US-08-458-568A-11	Sequen

ALIGNMENTS

RESULT 1
US-09-616-289-45
; Sequence 45, Application US/09616289
; Patent No. 6632923
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon M.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TRE
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/616,289
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1614
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1614)
US-09-616-289-45

Alignment Scores:
Pred. No.: 7.45e-100   Length: 1614

```
%:       2850.00      Matches:         538
%:       100.00%      Conservative:      0
%:       100.00%      Mismatches:        0
         100.00%      Indels:            0
rity:                 Gaps:              4

(1-538) x US-09-616-289-45  (1-1614)
```

```
         AlaGlyProProAlaLeuProProGluThrAlaAlaAlaAlaThrThrAlaAla  20
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
         GCGGGGCCCCCGGCCTTACCCCCGGAGACGGCGGCCGCCACCACGGCGGCC     60

         AlaSerSerAlaAlaSerProHisTyrGlnGluTrpIleLeuAspThrIleAsp  40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
         GCCTCGTCGCCGCTTCCCGCACTACCAAGAGTGGATCCTGGACACCATCGAC    120

         LeuArgSerArgLysAlaArgProAspLeuGluArgIleCysArgMetValArgArg  60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
         CTGCGCTCGCCAAGGCGCGGCCGACCTGGAGCGCATCTGCCGGATGGTGCGGCGG  180

         HisGlyProGlnProGluArgThrArgAlaGluLeuGlyLeuIleGlnGlnArg  80
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
         CACGGCCCGGAGCCGGAGCGCACGCGCGCCGAGCTGGAGAAACTGATCCAGCAGCGC  240

         ValLeuArgValSerTyrLysGlySerIleSerTyrArgAsnAlaAlaArgValGln  100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
         GTGCTCCGGGTCAGCTACAAGGGAGCATCTCGTACCGCACACGCGGCGCGCGTCCAG  300

         ProArgArgGlyAlaThrProProAlaProArgAlaProAlaGlyGlyAlaProAla  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
         CCCCGGCGCGGAGCCACCCCGCCCCCCGCCCCGCGGGGGCCCCGCC              360

         AlaAlaAlaAlaAlaProProThrProProAlaProProAlaProAlaProVal  140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
         GCGGCCGCCGCCGCGCCGCCCACGCCGCCCGCCCCGCCCCCGCCGCCCGTC         420

         AlaAlaAlaProAlaArgAlaProAlaAlaAlaAlaAlaAlaAlaThrAlaProPro  160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
         GCGGCCGCCCCGGCGCCCGCGGCGCCCGCCGCCGCCGCCCACCAGCGCCCCC         480

         ProGlyProAlaGlnProGlyProAlaGlyAlaGlnAlaAlaProLeuAlaProAla  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
         CCTGGCCCCGCGCAGCCGGGCCCCGCGGGGGCGCAGGCCGCGCCCCTGGCCCCGGCG  540

         ProAlaProAlaAlaProAlaProAlaValAlaProProAlaGlyProArgArgAlaPro  200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
         CCCGGCGCCAGCCGCTCCCCCGCGCGGCGTGGCCCCCGGCCGCCGCCGCCCCC        600

         ProAlaValAlaAlaAlaArgGluProProLeuProProGlnProProAlaPro  220
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
         CCCGCCGTTGCCGCCGGGAGCCGCCGCTACCCGCCGCCGCCGCCGCCGGCCG        660

         GlnGlnGlnGlnProProProGlnProGlnProGlnProGluGlyGlyAlaVal  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
         CAGCAGCAGCAGCCGCCGCCGCCGCAGCCACAGCCGCGCCGCGGGGGGCGCGGTG  720

         AlaGlyAlaAlaAlaArgProValSerLeuArgGluValValArgTyrLeuGlyGly  260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
         GCCGGCGCCGCGGCGCCCGTGAGCCTGCGGGAAGTCGTGCGCTACCTCGGGGGC     780

         GlyGlyAlaGlyGlyArgLeuThrArgGlyArgValGlnGlyLeuLeuGlnGluGlu  280
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
         GGCGGCGCCGGCGGCCGGCTCACCCGAGCCGCCGCTGCTGCAGGGGCGCAGGAGGAG  840

         AlaAlaAlaArgGlyArgGluArgThrArgLeuGlyAlaLeuAlaLeuProArgGly  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
         GCGGCTGGAGGCCGTCTCGGAGGCGCACCCGTTCGCGGCGCTTGCGCTGCCCCGCGGG  900

         ArgProGlyArgAlaProAlaAlaSerArgAlaArgProSerArgSerArgArgGly  320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
         AGGCCCGGACGGGCGCCGCGGCCCGCCGGGCCCGCCTCTCGCAGCAAGAGAGAGGT  960

         GluGluArgValLeuGluLeuLysGluGluGluGluLeuGluAspAspAspGluAspGlu  340
```

```
Db       |||||||||||||||||||||||||||||||||||||||||||||||||
         GGAGAAGAGGCGAGTACTTGAGAAAGAAGAAGAAGAGGAAGAGATGATGAAGATGAAAG

Qy   341 GluAspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyA
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 GAAGATGATGTGTCAGAGAGCTCTGAAGTGCCCGAGAGTGACCGTCCTGCGAGGTG

Qy   361 HisHisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluArgGlyValLysG
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 CACCACCAGCTTAACGGCGAACGGGGACCTCAGAGTGCCAAGGAGCGGGGTCAAGG

Qy   381 ThrProCysGlyProHisGlnGlyGlnAspGluArgGlyArgGlyProAlaProGlyLys
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 ACCCCCTGCGGACCGCACCAGGGCCAGGATGAAGGGCGGGGCCAGCCCCGGGCA

Qy   401 ThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerV
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 ACCCGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGAACAGCTTCTG

Qy   421 ThrGlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuP
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 ACCGGGCCAGACTCCCCGTCCCCGGTGCCTTTGCCCCCAGGCAAACCAGCCCTAC

Qy   441 AlaAspGlyThrProPheGlyCysProProProGlyArgLysGluProSerSerAspP
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 GCCGACGGGACCCCCTTGGCTGTCCGGCCCGGGCCAAAGAGAAGCCATCTGATC

Qy   461 GluTrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGluG
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 GAGTGGACCGTGATGATGTCGTCGAATATTTACTGAGGCTGGATTCCCGAGC

Qy   481 ThrAlaPheGlnGluGlnGlnIleAspGlyLysSerLeuLeuLeuMetGlnArgT
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 ACAGCTTTCCAAGAGCAGAAATTGATGGCAAATCTTTGCTGCTAATGCAGCGCA

Qy   501 ValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisH
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 GTGCTCACCGGCCTGTCCATCCGCCTCGGGCCCAGCCTGAAAATCTACGAGCACC

Qy   521 LysValLeuGlnGlnGlyHisPheGluAspAspArgProAspGlyPheLeuGlyY
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 AAGGTGCTTCAGCAAGGCCACTTTGAGGATGATGACCCCGATGGCTTCTTAGGC
```

```
RESULT 2
US-09-616-289-50
; Sequence 50, Application US/09616289
; Patent No. 6632923
; GENERAL INFORMATION:
;  APPLICANT: Lees, Ann M.
;  APPLICANT: Lees, Robert S.
;  APPLICANT: Law, Simon W.
;  APPLICANT: Arjona, Anibal A.
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;  TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREA
;  TITLE OF INVENTION: ATHEROSCLEROSIS
;  FILE REFERENCE: 10797-004001
;  CURRENT APPLICATION NUMBER: US/09/616,289
;  CURRENT FILING DATE:  2000-07-14
;  PRIOR APPLICATION NUMBER: US 09/517,849
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 08/979,608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US 60/031,930
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US 60/048,547
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 50
;  LENGTH: 12425
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-09-616-289-50
```

```
               Length:        12425
2.16e-90       Matches:       536
2616.50        Conservative:  0
ty:    69.16%  Mismatches:    2
arity: 69.16%  Indels:        239
       91.81%  Gaps:          4

(1-538) x US-09-616-289-50  (1-12425)
```

```
Db  3732  GACAGGCCCGGAGCGGGCGGCCGCCGCCGGCCGCGCCCCAGCGCCCGCCCCGTCTCGCAGCAA(
Qy   316  -----------------------------------------------------------------

Db  3792  GCGCCCGGGAGCGGGGCGGCCGCCGCCGGCGGTGGGCAGGTGCGGGGCGAAGTTGGTGG:
Qy   316  -----------------------------------------------------------------

Db  3852  GCGAGTCCCGGAGGAGAACTGGGTGGCGGGTGGCTGGGGCTTTGCGCGCGTTC
Qy   316  -----------------------------------------------------------------

Db  3912  CTCGGTGCGTGGTGACCTTGGCAAGTGATTGAATCTCCCGGAGCCTCAGTTTC
Qy   316  -----------------------------------------------------------------

Db  3972  GTAAACGCGGTTTAATAACAGTAGCGACCCCTTGGGGTTGTTGAGCGAGTTTA
Qy   316  -----------------------------------------------------------------

Db  4032  TTGGTTGTCGAGGGCTTTAGTTAACACAGAGCCTGGCACGAGTGAATGCCGTA
Qy   316  -----------------------------------------------------------------

Db  4092  GTCCGTATTGTTCTTAAAGGTGGAATCGGTTCCTCCTCCCCACCGCCCCGGACG
Qy   317  -----------------------------------------------------Se---

Db  4152  CAGGGTCTGGGATTAGAACAGCTACTAATTTTGCATGCTTTCTTCTCCTCGGCTC
Qy   320  GlyGlyGluGluArgValLeuGluLysGluGluGluGluAspAspAspGluAsp
Db  4211  GGTGGAAGAGCGAGTCACTTGAGAAGAAGAAGAAGAAGAGATGATGATGAAGA

Qy   340  GluGluAspAspValSerGluGlySerGluValProGluSerAspArgProAl
Db  4271  GAAGAAGATGATGTGTCAGAGGGCTTCGAAGTGCCCGAGAGTGACCGTCCTGCA

Qy   360  GlnHisHisGlnLeuAsnGlyGlyArgGlyProGlnSerAlaLysGluArgVa
Db  4331  CAGCACCACCAGCTTAACGGCGAGCGGGGACCTCAGAGTGCCAAGGAGAGGGT

Qy   380  TrpThrProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaPr
Db  4391  TGGACCCCCTGCGGACCGCACCAGGGCCAGGATGAGGGCGGGGCGCCAGCCCC

Qy   400  GlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyLyThr---
Db  4451  GGCACCCGCCAGGTGTTCTCCATGGCAGCCATGAACAAGAAGGGGAACAGGT

Qy   416  0
Db  4511  CCCTCTGGGTGGGAAGAGTGCTAGGTGGAGGAGAACTGACCCGAAGACAAA(

Qy   417  -----------------AlaSerValAlaThrGlyProAspSerProSe
Db  4571  ACAGGTGTTTTTTCCTTCCCAGCTTCTGTTGCCACCGGCCAGACTCCCCGTC

Qy   429  lProLeuProProGlyLyProGlyAlaLeuProGlyAlaAspGlyThrProPheG1
Db  4631  GCCTTTGCCCCAGGCAAACCAGCCCTACCTGGGCGCGACGGGACCCCCTTTGG

Qy   449  -----------------------------------------------------
Db  4691  GTAAGTTGGGGTATTGGGACACATGGGGTGCTGCTCAGGTGTGTGGTACAGCCA

Qy   450  ---------------------------------------ProGlyLysGlu1
Db  4751  CATCCGTGTTCACTGGTGTCGTTGTTTTGATGCAGTCCCGGGCGCAAAGAGA

Qy   457  erAspProValGluTrpThrValMetAspValValGluTyrPheThrGluAlaG
Db  4811  CTGATCCCGTCGAGTGGACCGTGATGGATGTCGTCGAATATTTTACTGAGGCTG
```

```
Qy   20   tAlaGlyProProAlaLeuProProGluThrAlaAlaAlaAlaThrThrAlaAla
Db  2891  GGGCGGGGCCCGGAGACGGCGGCCACCACGGCGGCC

Qy   40   aAlaSerSerAlaAlaSerProHisTyrGlnGluTrpIleLeuAspThrIleAsp
Db  2951  CGGCCTCGTGTCCCCGGCTTCCCCGCACTACCAAGAGTGGATCCTGGACACCATCGAC

Qy   60   rLeuArgSerArgLysAlaArgProAspLeuGluIleCysArgValValArgArg
Db  3011  GCTGCGCTTCGGCAAGGCGCGGCCCGACCTCGAGCGCATCTGCCGGATGGTGCGGCGG

Qy   80   gHisGlyProGluGluThrArgAlaGluLeuGluLysGluLeuGlnLnArg
Db  3071  GCACGGCCCGGAGGAGACGCGAGCCGAGCTCGAGAAACTGATCCAGCAGCGC

Qy   100  aValLeuArgValSerTyrLysGlySerIleSerTyrArgAsnAlaAlaArgValGln
Db  3131  CGTGCTCCGGGTCAGCTACAAGGGGAGCATCTCGTACCGCAACGCGGCGCGTCCAG

Qy   120  GlyGlyAlaThrProProAlaProProArgAlaProArgAlaGlyAlaProAla
Db  3191  GCCCCGGCGCGGAGCCCACCCCCGCCGCCCCGCGGGGCCCCGGGGCGCCCGCC

Qy   140  aAlaAlaAlaProProThrProAlaProProProProAlaProProVal
Db  3251  CGCCCGGCGCCCCCGCCGCCCCCGCGCCCCGCCCCGCCACCCGCCCGCGCCCGTC

Qy   160  aAlaAlaAlaProAlaArgAlaAlaProAlaAlaAlaAlaAlaAlaThrAlaProPro
Db  3311  CGCCGCCGCCCCCGGCGCCCCGCGCGGCCCGGCGCCCCCCAGCGCCCCCCC

Qy   180  rProGlyProAlaGlnProGlnProProGlnProProGluGluArgGlyProAlaPro
Db  3371  GCCTGGCCCCGCGCAGCCCGCGCAGCGCCACAGCGGCCCGCCGGGGCGCCGCG

Qy   200  oProAlaProAlaAlaProAlaValAlaProAlaGlyProArgArgAlaAlaPro
Db  3431  GCCCGGCCCCAGCCGCCTCCCCCAGGCGGTGGCCCCGGCCGGGCCGCCGCCCCC

Qy   220  oProAlaValAlaAlaAlaArgGluProLeuProProGlnProProProAlaPro
Db  3491  GCCCGGCCCGTGCGCGCCCCGGAGCGCCCCCTGCCGCGCCACAGCCGCCGGCCG

Qy   240  oGlnGlnGlnGlnProProGlnProProGlyGluGlyProGlyGlyAlaAlaVal
Db  3551  ACAGCAGCAGCAGCCGCCCCGCCCCAGCGCCGCCGGGAGCGGGGCGCGGTG

Qy   260  gAlaGlyGlyAlaAlaArgProValSerLeuArgArgGluValValAlaTyrLeuGlyGly
Db  3611  GGCCGGGCGGGCGGGGGCGCCCGAGCGTGCTGCGGCGGGAAGTCGTGGCGTACCTCGGGGGC

Qy   280  rGlyGlyAlaGlyLeuThrArgGlyLeuArgValGlnArgValGluLeuGlu
Db  3671  CGGCGGCGGGCCCGGGGTCGCCTAACCCCGCGGGCGGCCGTGCAGGGGCTGCGGGTGCAGCGAGTGGAGGAG

Qy   300  aAlaAlaArgGlyLeuGlnArgThrArgGlyLeuLeuAlaLeuLeuProArgGly
Db  3731  GGCGGCTCCGAGGGCGTCTGAGCGCACCCGTCTCGGAGCGCGCTTGCGCTGCCCCGGGG

Qy   316  pArgProGlyLyArgAlaProAlaAlaSerArgAlaArgProSerArg------
Db
```

```
Qy   40  AspSerLeuArgSerArgLysAlaArgProAspLeuGluArgIleCysArgMetV
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  366  GACTCGCTGCGTCGCCAAGGCGCGGCCGGACCTGGAGCGCATCTGCCGGATGG

Qy   60  ArgArgHisGlyProGluProGluArgThrArgAlaGluLeuGluLysLeuIleG
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  426  CGGCGGCACGGCCCGAGCCGGAGCGCACGGCGCGGAGCTCGAGAAACTGATCC

Qy   80  ArgAlaValLeuArgValSerTyrLysGlySerIleSerTyrArgAspAsnAlaA
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  486  CGGCGCGTGCTCCGGGTCAGCTACAAGGGAGCATCTGCTACCGGCAACGGCGC

Qy  100  GlnProArgArgGlyAlaThrProProAlaProProArgAlaProArgGlyA
         ||||||||||||||||||||||||||||||||||||||||||||
Db  546  CAGCCGCCCGGCGGCGGAGCCACCCCCGGCGCCCGGCGCCCCGGCGGGG

Qy  120  AlaAlaAlaAlaAlaAlaProProThrProAlaProProProProProA
         ||||||||||||||||||||||||||||||||||
Db  606  ------GCCGGCGCCCGGCGCCCCACGCCCCGCGCCGCCGCCGCCCCG

Qy  140  Val---AlaAlaAlaAlaProAlaAlaArgAlaProArg-----AlaAlaAlaAlaA
         |||                                          ||||
Db  660  GTCGCCGCCGGCGCCCGGCGCCCCGGGCGCGGCCGGCGCCGCCGCCGCTG

Qy  157  ThrAlaProProSerProGlyProAlaGlnProGlyProArgAlaGlnArgAlaA
         ||||||||||||||||||||||||||||||||||||||||||||
Db  720  ACAGCGCCCCCTCGCCCGGCCCGGCGCAGCCCGGCCCCCGCCAGCGGCCG

Qy  177  LeuAlaAlaAlaProProAlaProAlaAlaProAlaValAlaProProAlaG
         ||||||||||||||||||||||||||||||||||||||||||||
Db  780  CTGGCCGCGGCGCCGCCGGCCCCCGCGTCCCCCGGCGGCGGCCCCCGGCCG

Qy  197  ArgArgAlaProProPro-----AlaAlaAlaAlaArgGluProProLeuProP
         ||||||||||||                                      |||
Db  840  CGGCGCGCGCCCCCCCCGTGCCGCCGGAGTCGCCGCCGCTCGCCGC

Qy  215  ProGlnProProAlaProProGlnGlnGln-------------ProProP
         |||||||||||||||||||                       ||||
Db  900  CCACAGCCGCCGCCGCCGCCCCACAGCAGCAGCCCGCCGCCCACCGCCGC

Qy  230  GlnProGlnProProGlyGluProGlyAlaValArgAlaGlyGlyAlaAlaArgP
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  960  CAGCCACAGCCACGCCCCGCCGGAGGGCGGCGGCGGCGGCGGCCCCGGGCGGC

Qy  250  SerLeuArgGluValValArgTyrLeuGlyValSerGlyValGlyAlaGlyAlaArgL
         ||||||||||||||||||||||||||||||||||||||||||||||
Db 1020  AGCCTGCGGGAGGTCGTGCGCTACCTCGGGGTAGCAGCCGCGCGTGGCGGCGCC

Qy  270  ArgGlyArgValGlnGlyLeuLeuGluGluGluAlaAlaAlaArgGlyArgLeuG
         |||||||||||||||||||||||||||||||||||||||||||||
Db 1080  CGCGGCCGCGTGCAGGGTCTGCTGGAGGAGGAGGCGGCGGCCGGGCCGCCTGG

Qy  290  ThrArgLeuGlyAlaLeuAlaLeuProArgGlyArgAspArgProGlyArgAlaProP
         ||||||||||||||||||||||||||||||||||||||||||||
Db 1140  ACCGGTCTCGGAGCGCTTGCGCTCCGGGGACAGGCCCGACGGGCGCCAC

Qy  310  AlaSerArgAlaProSerArgLysArgGlyLyGlyGluGluGluValLeuGluLeuL
         ||||||::::|||||||||||||
Db 1200  GCCAGCGCCCGGCCGGCGGGAACAAGAGAGCTGGCAGAGAGCGAGTGCTTGAAA

Qy  330  GluGluGluAspAspAspAspAspGluGluAspAsp-----ValSerG
         ||||||::::::::::||||
Db 1260  GAGGAGGAGGAGGAGGAAGACGAAGACGACGACGTCGTGTCCG

Qy  348  SerGluValProGluSerAspArgProAlaGlyLyAlaGlnHisHisGlnLeuAsn-
         |||||||||||||||||||
Db 1320  TCGGAGGTGCCCGAGAGCGATCGTCCCCGGCGGCATCACCAGCTGAATG

Qy  367  GluArgGlyProGlnSerAlaLysGluArgValLysGluTrpThrProCysGlyP
         |||||||||:::|
Db 1380  GAGCGCGGCCCCAGACCCGCCAAGGAGTGGTGGCCTGGTGTGGCC

Qy  387  GlnGlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThrArgGlnValP
```

```
luGlnAlaThrAlaPheGlnGlu---                                 485
|||||||||||||||
AGCAGGCGACAGCTTTCCAAGA-GCAGGTGAGTTTCAGCCCAGGACTACACACTGA 4929

---                                                         485
ACACAGAGGGCCTCCCTGGGATGTGCCCTGATCCCGGCTTTCTCTGTTCCTGTTCCCA 4989

lnGlyIleAspGlyLysSerLeuLeuLeuMetGlnArgThrArgAspValLeuThrGlyL 505
|||||||||||||||||||||||||||
AGGAAATTGATGGCAAATCTTTGCTGCTCATGCAGCGCACAGATGTGCTCACCGGGC 5049

erIleArgLeuGlyTyrAlaLeuLysIleTyrGluHisHisIleLysValLeuGlnG  525
||||||||||||||||||||||||||
CCATCCGCCTCGGGCACGCCCTGAAAATCTACGAGCACCACATCAAGGTGCTTCAGC 5109

lyHisPheGluAspAspAspProAspGlyPheLeuGly 538
|||||||||||||||||
GCCACTTTGAGGATGATGACCCCGATGGCTTCTTAGGC 5150
```

```
         4.41e-90        Length:        2561
         2594.00         Matches:       503
y:       94.20%         Conservative:  17
rity:    91.12%         Mismatches:    16
         91.02%         Indels:        16
         4              Gaps:          8

(1-538) x US-09-616-289-48  (1-2561)
```

```
AlaGlyLyProAlaLeuProProGluThrAlaLaAlaAlaThrThr---Ala 19
||||||||||||||||||||||||||||||||||
GCGGGGCTGCCCCCCGGCCCTACCCCCCCGAGACGGCGGCGGCCACCACGGCCGCGG 305

AlaAlaSerSerSerAlaAlaSerProHisTyrArgGlnGluTrpIleLeuAspThrIle 39
|||||||||||||||||||||||||||||||
GCCGCCTCGTGTCCCGCGCGTTCCCCGCACTACCAAGAGTGATTCGGACACCATC 365
```

```
LENGTH: 1617 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-08-979-608A-11

Alignment Scores:
Pred. No.:                              1.81e-47        Length:         1617
Score:                                  1455.50         Matches:        281
Percent Similarity:                     92.86%          Conservative:   18
Best Local Similarity:                  87.27%          Mismatches:     13
Query Match:                            51.07%          Indels:         10
DB:                                     4               Gaps:           3

US-09-976-740-43 (1-538)  x  US-08-979-608A-11  (1-1617)

Qy  221 ProGlnGlnGlnProProProProGlnProProProGlnProPo-ProGluGlyGl
            ||||||::||||||||||||||||          ||||| :||
Db    6 CCGCAGCAGCAGCAA---------------------CAACCGCTAGCCGAAGGGTGC

Qy  240 lArgAlaGlyGlyAlaAlaArgProValSerLeuArgGluValValArgTyrLe
            |||||||||||||||||||||||||||||||||||||   :::||||
Db   48 GCGGGCCGGCGGCGGCCCGGCGCCGGTGAGCCTGCGGGAAGTGTGCGCGCTACCT

Qy  260 yArgSerGlyValAlaGlyIleGlyArgLeuThrArgGlyValGlnGlyLeuLeuGl
            ||||||:||||:|||||||||||||||||||||||||||||||||||||||||
Db  108 TAGCAGCGGCGTCGGCGGCGCCGGCCTGACCCGCGGCGCCGGTGCAGGGTCTGCTGGA

Qy  280 uAlaAlaAlaArgGlyAlaArgLeuGlnAlaThrArgLeuGlyLeuAlaLeuAlaLeuPr
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  168 GGCCGCGGCGCCGGCGGCCGGCCCGCGCCTGGAGGCGCACCCGTCTCGGAGCGTCGCTGCC

Qy  300 yAspArgProGlyArgAlaProAlaAlaSerAlaArgProSerArgSerLy
            |||||||||||||||||||||||||||            :::||||
Db  228 GGACAGGCCCGGACGGCGGCGCCACCGGCCCCGGCGCCGGCGCGGAACAA

Qy  320 yGlyGluGluArgValLeuGluValGluGluGluGluGluGluAspAspGluAspGlyGluAspGl
            ||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db  288 TGGCGGAGGAGCGAGTGCTTGAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAAGGACGA

Qy  340 uGluAspAsp------ValSerGluGlyValProGluSerAspArgPr
            ::::|||              ||||||||||||||||||||||||||||||||
Db  348 CGACGACGACGACCTCGTGTCCGAGGGCTTCGGAGGTGCCCGAGAGCGATCGTCC

Qy  358 yAlaGlnHisHisGlnLeuAsn---GlyGluArgGlyProGlnSerAlaLysGl
            ||||||||||||||:::          |||||||||||||||||||||||||
Db  408 TGCCAGCATCACCAGCTGAATGCGGCGCCCGGTGCCTGGCGGCGCCGCCGCCAGGA

Qy  377 lLysGluTrpThrProCysGlyTyrProHisGlnHisGlyGlnAspGluGlyArgGlyTyrPr
            |||||||  |||||:::          |||||||||||||||||||||||||||
Db  468 CAAGGAGTGGTCGCTGGTGTGGCCCCACCCTGGCCAGGAGGAGGAGCGGGGGGCC

Qy  397 oGlySerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGl
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  528 GGGCAGTGGCACCCGCCAGGTGTTCTCCATGGCGGCCTTGAGTAAGGAGGGGGG

Qy  417 aSerValAlaThrGlyTyrAspSerProSerProValProLeuProProGlyTyrPr
            ||||          |||||||||||||||||||||||||||||||||||||||||:::
Db  588 CTCTTCGACCACCGGCCTGACTCCCCGGTCCCCGGTGCCTTTGCCCCCGGGAA

Qy  437 aLeuProGlyAlaAlaAspGlyThrProPheGlyTyrCysProProGlyArgLysGlyLy:
            |||||||||||||||||||||||||||||||||||||||||||||:::||||
Db  648 CCTCCCAGGAGCCGATGGGACCCCCTTTGGCTGCCCTGCCCGGGCGCAAAGAGAA

Qy  457 rAspProValGluThrValMetAspValValGlyTyrPheThrGluAlaGl:
            :|||          ||||||||||||||||||||||||||||||||||||:::
Db  708 AGACCCCGTGGAGTGGACAGTCATGGACGTCGTGAGTACTTCACCGAGGCGGG

Qy  477 oGluGlnAlaThrAlaPheGlnGlyGlnGluIleAspGlyLysSerLeuLeu
            ||||||||||||||||:::||||:::          |||||||||||||||||
Db  768 TGAGCAAGCCACCGGCTTTCCAGGAGCAGGAGGATCGACGACGACGAAGTCCCTGCTGCT
```

Right-side continued sequence lines:

```
            ||||||::||||          ||||||||||||||||||||||||||||
TGGCCAGGAGGAAGGGCGGGGGGCCGGCCGCGGCCAGTGGCACCGCACCGGTGTTCTCC 1499

tAlaAlaMetAsnLysGluGlyGlyGlyThrAlaSerValAlaThrGlyProAspSerPro 426
            |||::::|||          ||||||||||||||||||||||||||||||||
GGCGGCCTTGAGTAAGGAGGGGGGGATCAGCCCTTTCGACCACCGGGGCCTGACTCCCCG 1559

rProValProLeuProProGlyLysProAlaLeuProGlyAlaAspGlyThrProPhe 446
            |||||||||||          |||||||||||||||||||||||||||||
CCCGGTGCCTTTGCCCCCGGGAAGCCAGCCCTCCCAGGAGCCGATGGGACCCCCTTT 1619

yCysProProGlyArgLysGluLysProSerAspProValGluThrValMetAsp 466
            |||||          |::||||||||||||||||||||||||||||||
CTGCCCTGCCCGGGCGCAAAGAGAAGCCGGCAGACCCCGTGGAGTGACAGTCATGGAC 1679

lValGluTyrPheThrGluAlaGlyGlnAlaThrAlaPheGlnGluGln 486
            ||||||||||          |||||||||||||||||||||||||||||
CGTGGAGTACTTCACCGAGGCGGGCCTTCCCTGAGCAAGCCACGGCTTTCCAGGAGCAG 1739

uIleAspGlyLysSerLeuLeuLeuMetGlnArgThrArgAspValLeuThrGlyLeuSer 506
            ||||||||||          |||||||||||||||||||||||||||||
GATCGACGGCCAAGTCCCTGCTGCTCATGCAGCGCACCGATGTCCTCACCGGCCTGTCC 1799

eArgLeuGlyProAlaLeuLysGlyIleTyrGluHisHisIleLysValLeuGlnGly 526
            |||||||||          |::|||||||||||||||||||||||||||
CCGCCTGGGGCCAGCGTTGAAAATCTCATGAGCACCATATCAAGGTGCTGCAGCAGGGT 1859

sPheGluAspAspAspAspGlyGluAspGlyPheLeuGly 538
            |||||          ||||||||||||||||
CTTCGAGGACGGACGGACGACCCGGAAGGCTTCCTGGGA 1895
```

```
Qy  240 lArgAlaGlyGlyAlaAlaArgProValSerLeuArgGluValValArgTyrLeu
            |||||||||||||||||||||||||||||||||||||  |||||||||||||||
Db   48 GCGGGCCGGCGGCCGGGCGGGGCCCTGAGCCTGGGGAGTCGTGCGCACCTC

Qy  260 ySerGlyTyrAlaAlaGlyGlyArgLeuThrArgGlyValArgValGlnGlyLeuLeuGlu
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  108 TAGCAGGCGGCGCTGGCGGGCCGCCTGACCCGCGGCCGCGTGCAGGTCTGCTGGAA

Qy  280 uAlaAlaAlaArgGlyArgLeuGluArgThrArgLeuGlyAlaLeuAlaLeuPro
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  168 GGGCGGCGGCGCGGGGCCCGGTCTCGGAGCGCTTCGCGGCGCTTGCGCTGCCC

Qy  300 yAspArgProGlyArgAlaProAlaAlaSerAlaArgProSerArgSerLys
            :::|||||||:|||||||||||||||||||||||||||||||||||||||||
Db  228 GGACAGGCCCGGACGGGCCGCCACCGGCCCCAGCGCCCGCGCGGGCGGAACAAG

Qy  320 yGlyGluGluArgValLeuGluLysGluGluAspAspGluAspAspGluAspGlu
            ||||||||||||||||||||||:|||::|||||||||||||||||||||||||
Db  288 TGGCGAGGAGCGAGTGCTTGAAAAGGAGGAGGAGGAGGAGGAGGAGGAAGACGAC

Qy  340 uGluAspAsp------ValSerGluGlySerGluValProGluSerGluArgArgPro
            :::|||||                |||||||||||||||||||||||||||||||
Db  348 CGAGCAGGACGACGTCGTGTTCCGGAGGCTCGGAGGTGCCCGGAGAGCGATCGTCCC

Qy  358 yAlaGlnHisHisGlnLeuAsn---GlyGluArgGlyTyrGlnSerAlaLysGlu
            |||||||||||||||||||||   ||||||||||||::::|||||||||||||||
Db  408 TGCCAGCATCACCAGCTGAATGGCGGGGAGCGCGGCGCCCCAGACGCCCAAGGAG

Qy  377 lLysGluTrpThrProCysGlyTyrProHisGlnGlnGlyGlnAspGluArgGlyTyrPro
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  468 CAAGGAGTGTCGCTGTGTGGCCCCACCCTGGCCAGGAGGAAGGGCGGGGGGGGCCG

Qy  397 oGlySerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGly
            |||||||||||||||||||||||||||:::::|||||||||||||||||||||||
Db  528 GGGCAGTGGCCACCCGCCAGGTGTTCCATGGCGGCCATGAACAAGGAGGGGGGA

Qy  417 aSerValAlaThrGlyProAspSerProSerProValProLeuProProGlyLys
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  588 CTCTTCGACCACCGGCCTGACTCCCCGTCCCCGTGCCTTTGCCCCCCGGAAG

Qy  437 aLeuProGlyAlaAspGlyThrProPheGlyCysProProGlyArgGlyLysGluLys
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  648 CCTCCCAGGAGCCGATGGAACCCCTTTGGCTGCCTGCCCTGCCCGGGGCCAAGAGAAG

Qy  457 rAspProValGluTrpThrValMetAspValValGluLeuTyrPheThrGluAlaGly
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  708 AGACCCCGTGGAGTGGACAGTCATGGACGTCGTGGAGTACTTCACCGAGGCGGGC

Qy  477 oGluGlnAlaThrAlaPheGlnGluGlnGluIleAspGlyLysSerLeuLeuLeu
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  768 TGAGCAAGCCACGGCTTTCCAGGAGCAGGAGATCGACGGGCAGTCCCTGCTGCTC

Qy  497 nArgThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIle
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  828 GCGCACCGATGTCTCCACCGGCCTGTCCATCCGCGTGGGGCCCAGCGTTGAAAATC

Qy  517 uHisHisIleLysValLeuGlnIleGlyHisPheGluGluAspArgAspGly
            :::|||||||||||||||||||||||||||||||||||||||||||::|||
Db  888 GCACCATATCAAGGTGCTGCAGACAGGTCACTTCGAGGAGGACGATGACCCGGAAGGC

Qy  537 uGly 538
        ||||
Db  948 GGGA 951
```

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Qy  ...ThrAspValThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGl 517
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  ...ACCGATGTCTCCACCGGCCTGTCCATCCGCCTGGGGCCCAGCGTTGAAAATCTATGA 887

Qy  ...HisIleLysValLeuGlnIleGlyHisPheGluGluAspAspArgAspGlyPheLe 537
        |||||||||||||||||||||||||||||:::|||||||||||||||||||||||
Db  ...CCATATCAAGGTGCTGCAGACAGGGTCACTTCGAGGAGGACGATGACCCGGAAGGCTTCCT 947

Qy  / 538
Db  \ 951
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            1.81e-47    Length:       1617
            1455.50     Matches:      281
Y:          92.86%      Conservative: 18
rity:       87.27%      Mismatches:   13
            51.07%      Indels:       10
            4           Gaps:         3
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```
(1-538) x US-09-517-849-11 (1-1617)

Qy  GlnGlnGlnProProProProGlnProProGluGlyGlyAlaVa 240
        ||||||||||||         |||::||||||||||||||||
Db  CAGCAGCAA---------CAACCCGTAGCCGAAGGGTGGCGCGGC 47
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Db 528 GGGCAGTGGCACCCGCCAGGTGTTCTCCATGCGGCCTTGAGTAAGGAGGGGG

Qy 417 aSerValAlaThrGlyProAspSerProValProLeuProProGlyL
||| |||||||||||||||||||||||||||||||||||||||||||
Db 588 CTCTTCGACCACCGGCCTGACTCCCCGGTGCCCCGGTGCCTTTGCCCCCGGGA

Qy 437 aLeuProGlyAlaAspGlyThrProPheGlyCysProProGlyArgGlyLysGluL
||||||||||||||||||||||||||||||||||||||||||||
Db 648 CCTCCCAGGAGCCGATGGGACCCCCCTTTGGCTGCCCTGCCGGGCGCAAAGAGA

Qy 457 rAspProValGluTrpThrValMetAspValValGluThrPheThrGluAlaG
:|||||||||||||||||||||||||||||||||||||||||||
Db 708 AGACCCCGTGGAGTGGACAGTCATGGACGTCGTGGAGTACTTCACCGAGGCGG

Qy 477 oGluGlnAlaThrAlaPheGlnGluGlnIleAspGlyLysSerLeuLeuL
||||||||||||||||||||||||||||||||||||||||||||
Db 768 TGAGCAAGCCACCGGCTTTCCAGAGACCAGGAGGAGGATCAAGTCCCTGCTGC

Qy 497 nArgThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysI
|||||||||||||||||||||||||||||||||||||||||||
Db 828 GCGCACCGATGTCCTCACCGGCCTGTCCATCCGCCTGGGCCCAGCGTTGAAAA

Qy 517 uHisHisIleLysValLeuGlnGlnGlyHisPheGluAspAspAspProAspG
|||||||||||||||||||||||||||||||||:::||
Db 888 GCACCATATCAAGGTGCTGCAGCAGGGTCACTTCGAGGACGATGACCCGGAAG

Qy 537 uGly 538
||||
Db 948 GGGA 951

RESULT 7
US-08-979-608A-13
; Sequence 13, Application US/08979608A
; Patent No. 6355451
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
;   Lees, Robert S.
;   Law, Simon W.
;   Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
;   BINDING PROTEINS AND THEIR USES IN DIA\
;   TREATING ATHEROSCLEROSIS

; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/979,608A
; FILING DATE: 26-No. 6355451-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/048,547
; FILING DATE: 03-JUN-1997
; APPLICATION NUMBER: US 60/031,930
; FILING DATE: 27-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1422 base pairs

ENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
ENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
ENTION: ATHEROSCLEROSIS
E: 10797-004001
CATION NUMBER: US/09/616,289
G DATE: 2000-07-14
ATION NUMBER: US 09/517,849
DATE: 2000-03-02
ATION NUMBER: US 08/979,608
DATE: 1997-11-26
ATION NUMBER: US 60/031,930
DATE: 1996-11-27
ATION NUMBER: US 60/048,547
DATE: 1997-06-03
Q ID NOS: 53
stSEQ for Windows Version 4.0

yctolagus cuniculus

).....(951)

:

        1.81e-47   Length: 1617
        1455.50   Matches: 281
ty: 92.86%   Conservative: 18
arity: 87.27%   Mismatches: 13
        51.07%   Indels: 10
        4   Gaps: 3

(1-538) x US-09-616-289-11 (1-1617)

oGlnGlnGlnGlnProProProProGlnProGlnPro-ProGluGlyGlyAlaVa 240
||||||||||||| ||||:::|||||||||||
GCAGCAGCAA-------------------CAACCGCTAGCCGGAAGGGTGGCGCGGC 47

rgAlaGlyGlyAlaAlaArgProValSerLeuArgGluValValArgTyrLeuGlyGl 260
|||||||||||||||||||||||||||||||||||||||||||||||||||
GGGCCGGCGCCCCGGCGCGCGCCCTGAGCCTGCGGGAAGTCGTGCGCTACCTCGGGGG 107

erGlyGlyAlaGlyGlyArgLeuThrArgGlyArgValGlnGlyValLeuLeuGluGluGluGlyGl 280
|||||||||||||||||||||||||||||||||||||||||||||||||||
GCAGCGGCGCTGGCGGCCCGGCCTGACCCGGCCGCGTGCAGGGTCTGTGGAAGAGA 167

laAlaAlaArgGlyArgGluArgThrArgLeuGlyValAlaLeuAlaLeuProArgGl 300
|||||||||||||||||||||||||||||||||||||||||||||||||||
CCGCGGCGGGGGGGGGGCCCTGAGCCGCACCCGTCTCGGAGCGGCTTGCGCTGCCCCGCGG 227

spArgProGlyArgAlaProAlaAlaSerAlaArgProSerArgSerLysArgGl 320
|||||||||||||||||||||| :::|||||||||||||||||||||
ACAGGCCCGGACGGGGCGCCACCGGCCCGCCCCCGCGGGCCCGGGACAACAGAGAGC 287

lyGluArgValLeuGluLysGluGluGluGluLysProGluProGluAspAspAspGluAspGl 340
||||||||||||||||||||||||||||||||:||||:::::::||
GCGAGGAGCGAGTGCTTGAAAAGGAGGAGGAGGAGGAGGAGGACGACGAGGA 347

luAspAsp-------ValSerGluGlySerGluValProGluSerAspArgProAlaGl 358
:||||| |||||||||||||||||||||||||||||:||
ACGACGACGACGTCGTGTCCGAGGGCTCGAGGTGCCGAGCGGATCGTCCCGCGGG 407

laGlnHisHisGlnLeuAsn---GlyGluArgGlyProGlnSerAlaLysGluAlaArgVa 377
|||||||||||||||| ||||||||||||||||||||||||||||
CGCAGCATCACCAGCTGAATGGGCGGCGAGCGCGCCCCGAGACCGCCAAGGAGCGGGGC 467

ysGluTrpThrProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyArgGlyProAlaPr 397
||||::: |||||:||||||||||||||||||||||||||||||||
AGGAGTGGTCGCTGTGTGGCCCCCACCCTGGCCAGGAGGAAGGGGCGGGGGGCCGGCCGC 527

lysSerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyLysGlyThrAl 417
||||||||||| ||||||:::::||||||||||||

; Sequence 13, Application US/09517849
; Patent No. 6605588
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; Lees, Robert S.
; Law, Simon W.
; Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
; BINDING PROTEINS AND THEIR USES IN DIAGN
; TREATING ATHEROSCLEROSIS
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/517,849
; FILING DATE: 02-Mar-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/979,608
; FILING DATE: 26-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10797-003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1422 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...756
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-517-849-13

Alignment Scores:
Pred. No.:   Length: 1422
Score: 1.35e-37   Matches: 223
                   1191.50   Conservative: 17
Percent Similarity: 95.24%   Mismatches: 9
Best Local Similarity: 88.49%   Indels: 3
Query Match: 41.81%   Gaps: 2
DB: 4

US-09-976-740-43 (1-538) x US-09-517-849-13 (1-1422)

Qy 290 ThrArgGlyValAlaLeuAlaLeuProArgGlyAspArgProGlyArgAlaPro/
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ACCCGTCTCGGAGCGCTTGCGCTGCCCGCGGGACAGGCCCGGACGGGCGCCA(

Qy 310 AlaSerAlaArgProSerLysArgGlyGlyGlyValLeuGlu/
          ||||||| :::|||||||||||||||||||||||||||||
Db   61 GCCAGCGCCGCGCGCGGAACAAGAGAGCTGGCGAGGAGCGAGGTGCTTGAAJ

Qy 330 GluGluGluAspAspAspGluAspGluuGluGlnAspAsp------ValSer(
          ||||:::::::||||| :::::::::|||||||||||||||
Db 121 GAGGAGGAGGAGGAGGAAGACGACGACGACGACGACACGTCGTGTCC(

Qy 348 SerGluValProGluSerAspArgProAlaGlyAlaGlnHisHisGlnLeuAsn-
          |||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db 181 TCGGAGGTGCCCGAGAGCGATCGTCCCGGCGGTGCGCAGCATCACCAGCTGAAT(

; B: nucleic acid
; ANDEDNESS: single
; OLOGY: linear
; E/KEY: Coding Sequence
; ATION: 1...756
; DESCRIPTION: SEQ ID NO: 13:

                   1.35e-37   Length: 1422
                   1191.50   Matches: 223
y: 95.24%   Conservative: 17
rity: 88.49%   Mismatches: 9
                   41.81%   Indels: 3
                   4   Gaps: 2

(1-538) x US-08-979-608A-13 (1-1422)

ArgLeuGlyAlaAlaLeuAlaLeuProArgGlyAspArgProGlyArgAlaProProAla   309
|||||||||||||||||||||||||||||||||||||||||||||||||||||||
CGTCTCGGAGCGCTTGCGCTGCCCGCGGGACAGGCCCGGACGGGCGCCACCGGCC   60

SerAlaArgProSerArgSerLysArgGlyGlyGlyValLeuGluValLeuLysGluLysGlu   329
||||||| :::|||||||||||||||||||||||||||||||||||||
AGCGCCCGCGCGCGCGGAACAAGAGAGCTGGCGAGGAGCGAGGTGCTTGAAAAGGAG   120

GluGluAspAspAspGluAspGluuGluAsp------ValSerGluGly   347
||||:::::::||||| :::::::::|||||||||||||||
GAGGAGGAGGAGGAGGAAGACGACGACGACGACGACACGTCGTCCGGAGGGC   180

GluValProGluSerAspArgProAlaGlyAlaGlnHisHisGlnLeuAsn---Gly   366
|||||||||||||:::||||||||||||||||||||||||||||||||
GAGGTGCCCGAGAGCGATCGTCCCGGCGGGTGCGCAGCATCACCAGCTGAATGGCGGC   240

ArgGlyProGlnSerArgAlaLysGluValLysGluValLysProTrpProCysGlyProHis 386
||||||||| :::|||||||||||||||||||||:::
CGGGGCCCGCAGAGCCGCGCCAAGGAGGCGGGCCAAGGAGTGGTCGCTGTGTGGCCCCCAC   300

GlyGlnAspGluGlyArgGlyTyrArgProGlySerGlyThrArgGlnValPheSer   406
||||||||||||||||||||||||||||||||||
GGCCAGGAGGAGGGCCGGGGCCGCCGCCCGGGCCAGTGGACCCGCCAGGTGTTCTCC   360

AlaAlaMetAsnLysGluGluGlyGlyThrAlaSerValAlaThrGlyProAspSerPro   426
|||||||||||||||||||||||||||||
GCGGCCTTGAGTAAGGAGGGGGGGATCAGCCTCTTCGACCACCGGCCTGACTCCCCG   420

ProValProLeuProProGlyLysProAlaLeuProGlyAlaAspGlyThrProPhe   446
|||||||||||||||||||||||||||||||
CCCGGTGCCCTTTGCCCCCCGGGAAGCCAGCCTCCCAGGAGCCGATGGGACCCCCCTTT   480

CysProProGlyArgLysGluLysProSerAspArgProValGluTrpProThrValMetAsp 466
|||||||||||| :::|||||||||||||||||||||||||||||
TGCCCTGCCGGGCCGCCAAGAGAGCCGGACGCCGCAGACCCCCGTTGGAGTGGACAGTCATGGAC 540

ArgLeuGlyProAlaLeuuLysIleTyrGluHisHisIleLysValLeuGlnGlnGly   526
|||||||||||||||||||||||||||||||
CGCCTGGGGCCAGCGTTGAAAATCTATGAGCACCATATCAAGGTGCTGCAGCAGGGT   720

PheGluAspAspProAspProGlyPheLeuGly   538
|||||||||||||||||||||
TTCGAGGACGACCATGACCCCGGAAGGGCTTCCTGGGA   756

Score: 1191.50   Matches: 223
Percent Similarity: 95.24%   Conservative: 17
Best Local Similarity: 88.49%   Mismatches: 9
Query Match: 41.81%   Indels: 3
DB: 4   Gaps: 2

US-09-976-740-43 (1-538) x US-09-616-289-13 (1-1422)

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Qy   290 ThrArgLeuGlyAlaLeuAlaLeuProArgGlyArgArgProGlyArgArgAlaPro
         ||||||:||||||||::|||||||||||||||||||||||||||||||||||||||||
Db     1 ACCCGTCTCGGAGCGTTGCGCTGCCCGCCCGGGGACAGGGCCCGGACGGGGCGGCCJ

Qy   310 AlaSerAlaArgProSerArgSerLysArgGlyGlyGlyValLysGluArgValLeuGlt
         |||||||||||||| :::|||||||||||||||||||||||||||||||||||||||
Db    61 GCCAGCGCCCGCCGGCGCGGAACAAGAGACGTGGCAGGGCGAGGAGCGAGTGCTTGAJ

Qy   330 GluGluGluGluGlyAspAspAspGluAspAsp------ValSer
         |||||||||||:|||||||||||||:|||||||      ||||
Db   121 GAGGAGGAGGAGGAAGACGACGAGGAAGACGACGACGAGCTGTGTCC

Qy   348 SerGluValProGluSerAspArgProValAlaGlyAlaGlnHisHisGlnLeuAsn
         ||||||||||||||:::|||||||||||||||||||||||||||||||||||||||
Db   181 TCGGAGGTGCCCGAGAGCGATCGTCCCGCGGGTGCGCAGCATCACCAGCTGAAT

Qy   367 GluArgGlyProGlnSerAlaLysGluArgValLysGluTrpThrProCysGly
         ||||||||||||||||||||||:::|||||||||||||||||||||:::||||
Db   241 GAGCGCGGCCCGCAGACCGCCAAGGAGAGGTGGTCGCTGTGTGGC

Qy   387 GlnGlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThrArgGlnVal
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CCTGGCCAGGAGGAAGGGCGGGGACCCGCGGGGCAGTGGCACCCGCCAGGTC

Qy   407 MetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThrGlyProAsp
         |||||:::::|||||||||||||||||||||||||||||||||||||||||||
Db   361 ATGGGGGCCTTGAGTAAGGAGGGGGGATCAGCCTCTTCGACCACCGGGCCTGAC

Qy   427 SerProValProLeuProProGlyValLysProAlaLeuProGlyAlaAspGlyThr
         ||||||||||||||||::|||||||||||||||||||||||||||||||||||||
Db   421 TCCCCGGTGCCCTTTGCCCCCGGGGAAGCCAGCCCCTTCCCAGAGACCGATGGGACC

Qy   447 GlyCysProProGlyArgGlyArgLysGlyLysProSerAspProValGluTrpThrVal
         |||||||||||||||||||||||||||||||||||||||||::||||||||||||||
Db   481 GGCTGCCCTGCCCGGCGCGGCCGCAAAGAGAAGCCGGCAGACCCCGTGGAGTGGACAGTC

Qy   467 ValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThrAlaPheGln
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GTCGTGGAGTACTTCACCGAGGCGGGCTTCCCTGAGCAAGCCACGGCTTTCCAG

Qy   487 GluIleAspGlyLysSerLeuLeuMetGlnArgThrAspValLeuThrGly
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GAGATCGACGGGAAGTCCCTGCTCATGCAGCGCACCGATGTCCTCACCGGC

Qy   507 IleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLysValLeuGln
         ||||||||||||||||||||||||::|||||||||:::|||||||||||||||
Db   661 ATCCGCCTGGGGCCAGCGTTGAAAATCATGAGCACCATATCAAGGTGCTGCAG

Qy   527 HisPheGluAspAspAspProAspGlyPheLeuGly 538
         |||||||||||||:::|||||||||||||||||||
Db   721 CACTTCGAGGACGATGACCCGGAAGGCTTCCTGGGA 756
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RESULT 10
US-08-979-608A-16
; Sequence 16, Application US/08979608A
; Patent No. 6355451
; GENERAL INFORMATION:
; APPLICANT: Leee, Ann M.
;   Lees, Robert S.
;   Law, Simon W.
;   Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
;   BINDING PROTEINS AND THEIR USES IN DIAG
;   TREATING ATHEROSCLEROSIS
;
; NUMBER OF SEQUENCES: 42
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uArgGlyProGlnSerAlaLysGluArgValLysGluTrpThrProCysGlyProHis 386
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GCGCGGCCCGCAGACCGCCAAGGAGAGCGGCCAAGGAGTGGTCGCTGTGTGGCCCCCAC 300

nGlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThrArgGlnValPheSer 406
|||::||:||||||||||||||||||||||||||||||||||||||||||||||||||
TGGCCAGGAGGAAGGGCGGGGGCGGCCCGGGGCAGTGGCACCCGCCAGGTGTTCTCC 360

tAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThrGlyProAspSerPro 426
|||||:::::|||||||||||||||||||||||||||||||||||::|||||||||||
GGCGGCCCTTGAGTAAGGAGGGGGGGGGATCAGCCCTCTTCGACCACCGGGCCTCCCCG 420

rProValProLeuProProGlyLysProAlaLeuProGlyAlaAspGlyThrProPhe 446
|||||||||||||||::|||||||||||||||||||||||||||||||||||||||||
CCCGGTGCCTTTGCCCCCGGGAAGCCAGCCCTCCCAGGAGCCGATGGGACCCCCTTT 480

yCysProProGlyArgGlyLysGlyLysProSerAspProValGluTrpThrValMetAsp 466
|||||| ||||||||::|||||||||||||||||||||||||||||||||||||||||
CTGCCCTGCCGCGGCCGCAAAGAGAAGCCGGCAGACCCCGTGGAGTGGACAGTCATGGAC 540

lValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThrAlaPheGlnGluIleAsp 486
||||||||||||||||||||::|||||||||||||||||||||||||||:::||||||||
CGTGGAGTACTTCACCGAGGCGGGCTTCCCTGAGCAAGCCACGGCTTTCCAGGAGCAG 600

uIleAspGlyLysSerLeuLeuMetGlnArgThrAspValLeuThrGlyLeuSer 506
|||||||||||||||||||||||||||||||||||||||||||||||||||||||
GATCGACGGCAAGTCCCTGCTCATGCAGCGCACCGATGTCCTCACCGGCCTGTCC 660

eArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLysValLeuGlnGlyHisGly 526
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sPheGluAspAspAspProAspGlyPheLeuGly 538
||||||||||||:::|||||||||||||||||||
CTTCGAGGACGATGACCCGGAAGGCTTCCTGGGA 756

pplication US/09616289
2923
ATION:
es, Ann M.
ees, Robert S.
aw, Simon W.
rjona, Anibal A.
NTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
NTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
NTION: ATHEROSCLEROSIS
B: 10797-004001
CATION NUMBER: US/09/616,289
G DATE: 2000-07-14
TION NUMBER: US 09/517,849
DATE: 2000-03-02
FION NUMBER: US 08/979,608
DATE: 1997-11-26
FION NUMBER: US 60/031,930
DATE: 1996-11-27
FION NUMBER: US 60/048,547
DATE: 1997-06-03
ID NOS: 53
tSEQ for Windows Version 4.0

yctolagus cuniculus

S
)...(756)

:   1.35e-37   Length: 1422
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NDENCE ADDRESS:
RESSEE: Fish & Richardson P.C.
EET: 225 Franklin Street
Y: Boston
TE: MA
NTRY: USA
: 02110-2804
READABLE FORM:
IUM TYPE: Diskette
PUTER: IBM Compatible
RATING SYSTEM: DOS
TWARE: FastSEQ for Windows Version 2.0
APPLICATION DATA:
LICATION NUMBER: US/08/979,608A
ING DATE: 26-No. 6355451-1997
PLICATION DATA:
LICATION NUMBER: US 60/048,547
ING DATE: 03-JUN-1997
LICATION NUMBER: US 60/031,930
ING DATE: 27-NOV-1996
/AGENT INFORMATION:
E: Myers, Louis
ISTRATION NUMBER: 35,965
ERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
UNICATION INFORMATION:
EPHONE: 617/542-5070
EFAX: 617/542-8906
OR SEQ ID NO: 16:
CHARACTERISTICS:
GTH: 1208 base pairs
E: nucleic acid
ANDEDNESS: single
OLOGY: linear

E/KEY: Coding Sequence
ATION: 1..651
DESCRIPTION: SEQ ID NO: 16:

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                7.64e-37          Length:       1208
                1170.00           Matches:       217
y:              100.00%           Conservative:    0
rity:           100.00%           Mismatches:      0
                41.05%            Indels:          0
                4                 Gaps:            0

(1-538) x US-08-979-608A-16 (1-1208)

        GluArgValLeuGluLysGluGluGluGluAspAspAspGluAspGluGlu 341
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        GAGCGAGTACTTGAGAAGAGAAGAGGAAGAAGATGATGAAGAAGATGAAGAA 60

        AspValSerGluGlySerGluValProGluSerAspArgProAlaGlyProAlaGlyAlaGlnHis 361
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        GlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluArgValLysGluTrpThr 381
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
        CAGCTTAACGGCGAGCGGGGACCTCAGAGTGCCAAGGAGAGGGTCAAGGAGTGGACC 180

        CysGlyProHisGlnGlnGlnAspGluGlyArgGlyArgGlyProAlaProGlySerGlyThr 401
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
        TGCGGACCGCACCAGGGCCAGGATGAAGGGCGGGGGCCAGCCCGGGCAGCGGGCACC 240

        GlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyGlyThrAlaSerValAlaThr 421
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
        CAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGAACAGCTTCTGTTGCCACC 300

        ProAspSerProValProLeuProProGlyLysProAlaLeuProGlyAla 441
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
        CCAGACTCCCCGTCCCCCGTGCCTTTGCCCCCAGGCAAACCAGCCCCTACCTGGGGCC 360
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RESULT 11
US-09-517-849-16
; Sequence 16, Application US/09517849
; Patent No. 6605588
- GENERAL INFORMATION:
- APPLICANT: Lees, Ann M.
-            Lees, Robert S.
-            Law, Simon W.
-            Arjona, Anibal A.
- TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
-            BINDING PROTEINS AND THEIR USES IN DIAG
-            TREATING ATHEROSCLEROSIS
- NUMBER OF SEQUENCES: 42
- CORRESPONDENCE ADDRESS:
- ADDRESSEE: Fish & Richardson P.C.
- STREET: 225 Franklin Street
- CITY: Boston
- STATE: MA
- COUNTRY: USA
- ZIP: 02110-2804
- COMPUTER READABLE FORM:
- MEDIUM TYPE: Diskette
- COMPUTER: IBM Compatible
- OPERATING SYSTEM: DOS
- SOFTWARE: FastSEQ for Windows Version 2.0
- CURRENT APPLICATION DATA:
- APPLICATION NUMBER: US/09/517,849
- FILING DATE: 02-Mar-2000
- PRIOR APPLICATION DATA:
- APPLICATION NUMBER: 08/979,608
- FILING DATE: 26-NOV-1997
- ATTORNEY/AGENT INFORMATION:
- NAME: Myers, Louis
- REGISTRATION NUMBER: 35,965
- REFERENCE/DOCKET NUMBER: 10797-003001
- TELECOMMUNICATION INFORMATION:
- TELEPHONE: 617/542-5070
- TELEFAX: 617/542-8906
- INFORMATION FOR SEQ ID NO: 16:
- SEQUENCE CHARACTERISTICS:
-   LENGTH: 1208 base pairs
-   TYPE: nucleic acid
-   STRANDEDNESS: single
-   TOPOLOGY: linear
- FEATURE:
-   NAME/KEY: Coding Sequence
-   LOCATION: 1..651
- SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-517-849-16

Alignment Scores:
Pred. No.:   7.64e-37   Length: 1208
Score: 1170.00   Matches: 217

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Qy  442 AspGlyThrProPheGlyCysProProGlyArgLysGluLysProSerAspPro'
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Db  361 GACGGGACCCCTTTGGCTGTCCTCCCGGGCGCAAAGAGAAGGAAGCCATCTGATCCC(

Qy  462 TrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGluGln
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 TGGACCGTGATGGATGTCGTCGAATATTTACTGAGGCTGGATTCCCGGAGCAG(

Qy  482 AlaPheGlnGluGlnGluIleAspGlyLysSerLeuLeuLeuMetGlnArgThr
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 GCTTTCCAAGAGCAGGAAATTGATGGCAAATCTTTGCTGCTCATGCAGCGCACA(

Qy  502 LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHis
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 CTCACCGGCCTGTCCATCCGCCTCGGGCCAGCCCTGAAAATCTACGAGCACCAC/

Qy  522 ValLeuGlnInGlyHisPheGluAspGluAspAspProAspGlyPheLeuGly  53(
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 GTGCTTCAGCAAGGCCACTTTGAGGATGATGATGACCCCGATGGGCTTCTTAGGC  65:
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;   PRIOR FILING DATE: 1997-06-03
;   NUMBER OF SEQ ID NOS: 53
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 16
;     LENGTH: 1208
;     TYPE: DNA
;     ORGANISM: Homo sapiens
;     FEATURE:
;       NAME/KEY: CDS
;       LOCATION: (1)...(651)
US-09-616-289-16

Alignment Scores:
Pred. No.:                          Length:              1208
Score:                  7.64e-37    Matches:             1170.00
Percent Similarity:     100.00%     Conservative:        217
Best Local Similarity:  100.00%     Mismatches:          0
Query Match:            41.05%      Indels:              0
DB:                     4           Gaps:                0
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US-09-976-740-43 (1-538)  x  US-09-616-289-16 (1-1208)
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Db      1  GAAGAGCGAGTACTTGAGAAAGAAGAGGAAGAAGATGATGAAGATGAAGAT

Qy    342  AspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAla
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  GATGATGTGTCAGAGGGCTCTGAAGTGCCCGAGACGTGACCCTGCAGGTGCC

Qy    362  HisGlnLeuAsnGlyLeuArgGlyProGlnSerAlaLysGluArgValLysGlu
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  CACCAGCTTAACGGCGAGCGGGGACCTCAGAGTGCCAAGGAGAGGGTCAAGGAC

Qy    382  ProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGlySer
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  CCCTGCGGACCGCACCAGGGCCAGGATGAAGGGGCGGGGCCCAGCCCCGGGCAGC

Qy    402  ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerVal
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  CGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGAACAGCTTCTGTT

Qy    422  GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuPro
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  GGGCCAGACTCCCCGTCCCCCGTGCCTTTGCCCCCAGGCAAACCAGCCCTACCT

Qy    442  AspGlyThrProPheGlyCysProProGlyArgGlyLysGluLysProSerAspPro
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  GACGGGACCCCCTTTGGCTGTCCTCCCGGGCGCAAAGAAGAAGCCATCTGATCCC

Qy    462  TrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGlyGln
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  TGGACCGTGATGGATGTCGTCGAATATTTTACTGAGGCTGGATTCCCGGAGCAG

Qy    482  AlaPheGlnGluGlnGluIleAspGlyLysSerLeuLeuLeuMetGlnArgThr
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    502  LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHis
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  CTCACCGGCCTGTCCATCCGCCTCGGGCCCGCCCTGAAAATCTACGAGCACCAC

Qy    522  ValLeuGlnGlnGlyHisHisPheGluAspAspAspProAspGlyPheLeuGly 53
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RESULT 13
US-08-979-608A-12
;  Sequence 12, Application US/08979608A
;  Patent No. 6355451
;  GENERAL INFORMATION:
;    APPLICANT: Lees, Ann M.
;               Lees, Robert S.
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ty:      100.00%      Conservative:   0
arity:   100.00%      Mismatches:     0
         41.05%       Indels:         0
         4            Gaps:           0

(1-538)  x  US-09-517-849-16  (1-1208)

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pAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHis 361
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sGlnLeuAsnGlyLeuArgGlyProGlnSerAlaLysGluArgValLysGluTrpPro 381
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CCAGCTTAACGGCGAGCGGGGACCTCAGAGTGCCAAGGAGAGGGTCAAGGAGTGGACC 180

oCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThr 401
||||||||||||||||||||||||||||||||||||||||||||||||
CTGCGGACCGCACCAGGGCCAGGATGAAGGGGCGGGGCCCAGCCCCGGGCAGCGGCACC 240

gGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThr 421
|||||||||||||||||||||||||||||||||||||||||||||||||
CCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGAACAGCTTCTGTTGCCACC 300

yProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAla 441
|||||||||||||||||||||||||||||||||||||||||||||||||
GCCAGACTCCCCGTCCCCCGTGCCTTTGCCCCCAGGCAAACCCTACCTGGGGGC 360

pGlyThrProPheGlyCysProProGlyArgGlyLysGluLysProSerAspProValGlu 461
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CGGGACCCCCTTTGGCTGTCCTCCCGGGCGCAAAGAAGAAGCCATCTGATCCCGTCGAG 420

oThrValMetAspValValGluTyrPheThrGluAlaGlyGlnAlaThr 481
|||||||||||||||||||||||||||||||||||||||||||||||||
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aPheGlnGluGlnGluIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspVal 501
|||||||||||||||||||||||||||||||||||||||||||||||||
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aThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLys 521
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ACCGGCCTGTCCATCCGCCTCGGGCCCGCCCTGAAAATCTACGAGCACCACATCAAG 600

LeuGlnGlnGlyHisHisPheGluAspAspAspProAspGlyPheLeuGly 538
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CTTCAGCAAGGCCACTTGGAGGATGATGACCCCGATGGCTTCTTAGGC 651
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Law, Simon W.
  Arjona, Anibal A.
INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
          BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
          TREATING ATHEROSCLEROSIS
F SEQUENCES: 42
NDENCE ADDRESS:
RESSEE: Fish & Richardson P.C.
BET: 225 Franklin Street
Y: Boston
TE: MA
NTRY: USA
: 02110-2804
 READABLE FORM:
IUM TYPE: Diskette
PUTER: IBM Compatible
RATING SYSTEM: DOS
TWARE: FastSEQ for Windows Version 2.0
APPLICATION DATA:
LICATION NUMBER: US/08/979,608A
ING DATE: 26-No. 6355451-1997
PLICATION DATA:
LICATION NUMBER: US 60/048,547
ING DATE: 03-JUN-1997
LICATION NUMBER: US 60/031,930
ING DATE: 27-NOV-1996
/AGENT INFORMATION:
E: Myers, Louis
ISTRATION NUMBER: 35,965
ERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
UNICATION INFORMATION:
EPHONE: 617/542-5070
EFAX: 617/542-8906
OR SEQ ID NO: 12:
CHARACTERISTICS:
GTH: 1362 base pairs
E: nucleic acid
ANDEDNESS: single
OLOGY: linear

E/KEY: Coding Sequence
ATION: 1..696
DESCRIPTION: SEQ ID NO: 12:

        1.15e-33   Length: 1362
        1086.50   Matches: 203
y: 94.83%   Conservative: 17
rity: 87.50%   Mismatches: 9
        38.12%   Indels: 3
        4   Gaps: 2

(1-538) x US-08-979-608A-12 (1-1362)

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GluGluAspAspAspGluAspGluAspGlu-----ValSerGluGly 347
  :|||||:::|||||:|||||||||||:||| |||||||||||
GAGGAGGAGGAGGAAGACGACGAGGACGACGACGACTCGTGTCCGAGGGC 120

GluValProGluSerAspArgProAlaGlyAlaGlnHisHisGlnLeuAsn--Gly 366
  :||||||||:||||:|||:::|||::|::|::|||| |||
GAGGTGCCCGAGGAGCGATCGTCCCGGCGTGCGCAGCATCACCAGCTGAATGGCGGC 180

ArgGlyProGlnSerAlaLysGluArgValLysGluTrpThrProCysGlyProHis 386
  |||||:::|||:::|:   :||:::::||||||||||||||||||||||||||
CGCGGCCCCGCAGACCGCCAAGGAGCGGGCCAAGGAGTGGTCCTGTGTGGGCCCCCAC 240

GlyGlnAlaAspGluGlyGlyArgGlyProAlaProGlyTyrSerGlyThrArgGlnValPheSer 406
  |||:||||||||| |||||||||||||||||||

APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TR
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 1362
TYPE: DNA
ORGANISM: Oryctolagus cuniculus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(696)
US-09-616-289-12

Alignment Scores:
Pred. No.:   1.15e-33   Length: 1362
Score: 1086.50   Matches: 203
Percent Similarity: 94.83%   Conservative: 17
Best Local Similarity: 87.50%   Mismatches: 9
Query Match: 38.12%   Indels: 3
DB: Gaps: 2

US-09-976-740-43 (1-538) x US-09-616-289-12 (1-1362)

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Qy 330 GluGluGluAspAspAspAspGluAspAspGluGluAspAsp------ValSe
Db   61 GAGGAGGAGGAGGAGGAAGACGACGACGACGACGACGAGCGTCGTGTC

Qy 348 SerGluValProGlnSerAspArgProAlaGlyAlaGlnHisHisGlnLeuAs
Db 121 TCGGAGGTGCCCGAGCAGGATCGTCCCCGGGGTGCGCAGCATCACCAGCTGAA

Qy 367 GluArgGlyProGlnSerAlaLysGluArgValLysGluTrpThrProCysGl
Db 181 GAGCGGCGCCCCAGACCGCCAAGGAGCGGGCCAAGGAGTGTCGCGTGTGG

Qy 387 GlnGlyGlnAspGluGlyArgGlyArgGlyProAlaProGlySerGlyThrArgGlnVa
Db 241 CCTGGCCAGGAGGAAGGGCGGGGGCCGGCCAGTGGCACCCGCCAGGT

Qy 407 MetAlaAlaMetAsnLysAsnLysGluGlyGlyThrAlaSerValAlaThrGlyProAsp
Db 301 ATGGCCGCCTTGAGTAAGGAGGGGGATCAGCCTCTTCGACCACCGGCCTGA

Qy 427 SerProValProLeuProProGlyLysProAlaLeuProGlyAlaAspGlyThr
Db 361 TCCCCGGTGCCTTGCCCCCGGGAAGCCAGCCCTCCAGGAGCCGATGGGAC

Qy 447 GlyCysProProGlyArgLysGluLysProSerAspProValGluTrpThrVal
Db 421 GGCTGCCCTGCCGGGCGCAAAGAGAGCCGGCAAGACCCCCGTGGAGTGGACAGT

Qy 467 ValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThrAlaPheGl
Db 481 GTCGTGGAGTACTTCACCGAGCGCGGCTTCCCTGAGCAAGCCACGGCTTTCCA

Qy 487 GluIleAspGlyLysSerLeuLeuMetGlnArgThrAspValLeuThrGly\

POLOGY: linear
ME/KEY: Coding Sequence
CATION: 1..696
E DESCRIPTION: SEQ ID NO: 12:

:   1.15e-33   Length: 1362
                  1086.50   Matches: 203
ty: 94.83%   Conservative: 17
arity: 87.50%   Mismatches: 9
                  38.12%   Indels: 3
                                  Gaps: 2

(1-538) x US-09-517-849-12 (1-1362)

aSerAlaArgProSerArgSerLysArgGlyGlyGluGluArgValLeuGluLysGlu 329
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CAGCGCCCGCCGCGGCCGGAACAAGAGAGCTGGCCGAGGAGGAGTGCTTGAAAAAGGAG 60

uGluGluGluAspAspAspAspGluAspGluAspAsp------ValSerGluGlyLy 347
    :::::::::::::::
GGAGGAGGAGGAGGAGGAGGACGACGACGACGACGACGACTCGTGTCCGAGGGC 120

rGluValProGluSerAspArgProAlaGlyAlaGlnHisHisGlnLeuAsn--Gly 366
   :::::::::::
GGAGGTGCCCGAGCAGGCAATCGTCCCCGGGGTGCGCAGCATCACCAGCTGAATGGCGGC 180

uArgGlyProGlnSerAlaLysGluArgValLysGluTrpThrProCysGlyProHis 386
   :::::::::::::
GGCGGCGCCCCAGACCGCCAAGGAGCGGGCCAAGGAGTGGTCGCGTGTGGCCCCCAC 240

nGlyGlnAspGluGlyArgGlyArgGlyProAlaProGlySerGlyThrArgGlnValPheSer 406
   ::::::::::::
TGGCCAGGAGGAAGGGCGGGGGCCGGCCAGTGGCACCCGCCAGGTGTTCTCC 300

tAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThrGlyProAspSerPro 426
   ::::::::::::
GGCGGCCTTGAGTAAGGAGGGGGATCAGCCTCTTCGACCACCGGCCTCCCCG 360

rProValProLeuProProGlyLysProAlaLeuProGlyAlaAspGlyThrProPhe 446
   ::::::::::::
CCCGGTGCCTTTGCCCCCGGGAAGCCAGCCCTCCAGGAGCCGATGGGACCCCCTTT 420

yCysProProGlyArgLysGluLysProSerAspProValGluTrpThrValMetAsp 466
   :::::::::::::
CTGCCCTGCCGGGCGCAAAGAGAGCCGGCAGACCCCGTGGAGTGGACAGTCATGGAC 480

lValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThrAlaPheGlnGluGln 486
   ::::::::::::
CGTTGGAGTACTTCACCGAGGCGGGCTTCCCTGAGCAAGCCACGGCTTTCCAGGAGCAG 540

uIleAspGlyLysSerLeuLeuMetGlnArgThrAspValLeuThrGlyLeuSer 506
   ::::::::::::
GATCGACGGCAAGTCCCTGCTCATGCAGCGCACCGATGTCCTCACCGGCCTGTCC 600

eArgLeuGlyProAlaLeuLysIleTyrGluHisIleLeuLysValLeuGlnGlnGly 526
   ::::::::::::
CCGCCTGGGCCCAGCGTTGAAAATCTATGAGCACCATATCAAGGTGCTGCAGCAGGGT 660

sPheGluAspAspAspProAspGlyPheLeuGly 538
   :::::::
CTTTCGAGGACGATGACCCGGAAGGCTTCCTGGGA 696

pplication US/09616289
2923
ATION:
ees, Ann M.
ees, Robert S.
aw, Simon W.

```
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCGACGGCAAGTCCCTGCTGCTCATGCAGCGGCACCGATGTCCTCACCGGCCTGTCC  600

ArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLysLysValLeuGlnGlnGly  526
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CGCCTGGGGCCAGCGTTGAAAATCTATGAGCACCATATCAAGGTGCTGCAGCAGGGT  660

PheGluAspAspAspProAspGlyPheLeuGly  538
||||||||||||||||||||||:::||||||||
TTCGAGGACGATGACCCCGGAAGGCTTCCTGGGA  696
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March 13, 2004, 04:07:02
6 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

...leic search, using frame_plus_p2n model

March 12, 2004, 20:46:42 ; Search time 778.355 Seconds
                           (without alignmentB)
                           2544.725 Million cell updates/sec

US-09-976-740-43
2850
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BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop   6.0 , Delext   7.0

2432557 seqs, 1840798884 residues

hits satisfying chosen parameters: 4865114

ength: 0
ength: 2000000000

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

is the number of results predicted by chance to have a
ter than or equal to the score of the result being printed,
ived by analysis of the total score distribution.

SUMMARIES

Query
Match Length DB ID   Description

No.	Length	%	Residues		Seq ID	
1	2850	100.0	1614	9	US-09-976-740-45	Sequenc
2	2850	100.0	1614	12	US-10-671-242-45	Sequen
3	2850	100.0	1614	13	US-10-023-529-45	Sequen
4	2850	100.0	1614	13	US-10-023-523-45	Sequen
5	2850	100.0	1614	15	US-10-616-187-45	Sequenc
6	2616.5	91.8	12425	12	US-09-976-740-50	Sequenc
7	2616.5	91.8	12425	13	US-10-671-242-50	Sequen
8	2616.5	91.8	12425	13	US-10-023-529-50	Sequen
9	2616.5	91.8	12425	13	US-10-023-523-50	Sequen
10	2616.5	91.8	12425	15	US-10-616-187-50	Sequen
11	2594	91.0	2561	9	US-09-976-740-48	Sequenc
12	2594	91.0	2561	12	US-10-671-242-48	Sequen
13	2594	91.0	2561	13	US-10-023-529-48	Sequen
14	2594	91.0	2561	13	US-10-023-523-48	Sequen
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16	1470	51.6	1445	10	US-09-945-527-6	Sequen
17	1455.5	51.1	1617	9	US-09-962-055-11	Sequen
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21	1455.5	51.1	1617	13	US-10-023-523-11	Sequen
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24	1191.5	41.8	1422	9	US-09-962-055-13	Sequenc
25	1191.5	41.8	1422	9	US-09-976-740-13	Sequenc
26	1191.5	41.8	1422	12	US-10-671-242-13	Sequen
27	1191.5	41.8	1422	13	US-10-023-529-13	Sequen
28	1191.5	41.8	1422	13	US-10-023-523-13	Sequen
29	1191.5	41.8	1422	15	US-10-616-187-13	Sequen
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31	1170	41.1	1208	9	US-09-976-740-16	Sequenc
32	1170	41.1	1208	12	US-10-671-242-16	Sequen
33	1170	41.1	1208	13	US-10-023-529-16	Sequen
34	1170	41.1	1208	13	US-10-023-523-16	Sequen
35	1170	41.1	1208	15	US-10-616-187-16	Sequen
36	1086.5	38.1	1362	9	US-09-962-055-12	Sequenc
37	1086.5	38.1	1362	9	US-09-976-740-12	Sequen
38	1086.5	38.1	1362	12	US-10-671-242-12	Sequen
39	1086.5	38.1	1362	13	US-10-023-529-12	Sequen
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41	1086.5	38.1	1362	15	US-10-616-187-12	Sequen
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ALIGNMENTS

RESULT 1
US-09-976-740-45
; Sequence 45, Application US/09976740
; Publication No. US20020194633A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TRE
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/976,740
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53

SEQ for Windows Version 4.0

p sapiens

...(1614)

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	100.00%	Conservative:	0	
rity:	100.00%	Mismatches:	0	
	100.00%	Indels:	0	
	9	Gaps:	0	

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       GCGGGGCGGCCCGGCGGTGCCTAACCCGCGGCGGCTGAGGGGCTGCTGAGC  781

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RESULT 2

DATE: 2000-03-02
ATION NUMBER: US 08/979,608
DATE: 1997-11-26
ATION NUMBER: US 60/031,930
DATE: 1996-11-27
ATION NUMBER: US 60/048,547
DATE: 1997-06-03
2 ID NOS: 53
tSEQ for Windows Version 4.0

mo sapiens

).....(1614)

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5.74e-144
2850.00          Length:        1614
100.00%          Matches:       538
ty:   100.00%    Conservative:  0
arity: 100.00%   Mismatches:    0
12               Indels:        0
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(1-538) x US-10-671-242-45 (1-1614)

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aAlaSerSerAlaAlaSerProHisTyrGlnGluTrpIleLeuAspThrIleAsp   40
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CGCCTCGTCGTCCGCCTTCCCCGCCACTACCAAGAGTGGATCCTGGACCACCATCGAC  120

rLeuArgSerArgLysAlaArgProAspLeuGluArgIleCysArgMetValArgArg   60
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gHisGlyProGluProGluArgThrArgAlaGluLeuGluLysLeuIleGlnGlnArg   80
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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aAlaAlaAlaAlaAlaProProThrProAlaProProProAlaProProAlaProProVal  140
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   721  CGGGCCGGCGCGGCCGGCCGGCCGGCCGTGAGCGTGCGGGAAGTCGTGCGCTACCT
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Db   841  GCGGGCGGCTCGAGGGCCGTTCGGAGGCGCACCCGTCTCGGAGGCGCTTGCGCTGCC
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Qy   301  AspArgProGlyArgAlaProProAlaAlaSerAlaAlaArgProSerArgSerLy
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Db   901  GACAGGCCCGGACACGGCGCCGCCGGCCCCGGCGCCCCCGTCTCCGCAGCAA
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Db   961  GGAGAAGAGCGGAGTACTTGAGAAAGAAGAAGAAGAAGAAGATGATGAAGATGA
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Qy   341  GluAspAspValSerGlyValProGluGlySerGluValProGluSerAspArgProAlaGl
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  GAAGATGATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCCTGCAGG
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Db  1141  ACCCCCTGCGACCGACCAGGGCCAGGATGAAGGGCGGGGGCCAGCCCCGGG
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   401  ThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSe
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Qy   421  ThrGlyProAspSerProSerProValProLeuProProGlyLysProAlaLeu
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Db  1261  ACCGGGCCAGACTCCCCGTCCCCGTGCCTTTGCCCCAGCGCAAACCAGCCCTA
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Qy   441  AlaAspGlyThrProPheGlyCysProProGlyArgLysGluLysProSerAsp
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Db  1321  GCCGACGGACCGGACCCCCTTGGCTGTCCGCCCGGGCGCAAAGAGAAGCCATCTGAT
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   461  GluTrpThrThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGl
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Db  1381  GAGTGGACCACGGTGATGGATGTCGTCGAATATTTTACTGAGGCTGGATTCCCGGAC
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Qy   481  ThrAlaPheGlnGluGlnGlnIleAspGlyLysSerLeuLeuLeuMetGlnArg
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Qy   501  ValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis
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Db  1501  GTGCTCACCGGCCTGTCCATCCGGCCTCGGGCCAGCCTGAAAATCACGAGCAC
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   521  LysValLeuGlnInGlyLysHisPheGluAspAspAspProGlyPheLeuGly
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RESULT 3
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; Sequence 45, Application US/10023529
; Publication No. US20020129388A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TION: ATHEROSCLEROSIS
: 10797-004001
ATION NUMBER: US/10/023,529
  DATE: 2001-12-17
ION NUMBER: 09/616,289
ATE: 2000-07-14
ION NUMBER: US 09/517,849
ATE: 2000-03-02
ION NUMBER: US 08/979,608
ATE: 1997-11-26
ION NUMBER: US 60/031,930
ATE: 1996-11-27
ION NUMBER: US 60/048,547
ATE: 1997-06-03
ID NOS: 53
SEQ for Windows Version 4.0

o sapiens

...(1614)

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y:       100.00%        Conservative:    0
rity:    100.00%        Mismatches:      0
         100.00%        Indels:          0
         13             Gaps:            0
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(1-538) x US-10-023-529-45 (1-1614)

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    AlaSerSerSerAlaAlaSerProHisTyrGlnGluTrpIleLeuAspThrIleAsp       40
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    LeuArgSerArgLysAlaArgProAspLeuGluArgIleCysArgMetValArgArg       60
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    CTGGCTCGCGCAAGGCGCGGGACCTGGAGCGCATCTGCCGGATGGTGCGGCGG          180

    HisGlyProGluProGluArgThrArgAlaGluLeuGluLysLeuGlnGlnArg          80
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    CACGGCCCGGAGCCGGAGCGCACGCGGGCGGAGCTCGAGAAACTCCAGCAGCGC        240

    ValLeuArgValSerTyrLysGlySerIleSerTyrArgAsnAlaAlaAlaValGln      100
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    CCCCGGCGGAGGCGCCACCCCCGCCGCCCGCCGCCGCGGAGGCGGCCCCCGCC         360

    AlaAlaAlaAlaAlaProThrProProThrProAlaProProProAlaProAlaProVal  140
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    GCGGCCGCCGCCGCGCCCGCCCCACGCCCCGCCGCCCGGCGCCCCGGCCCCGTC        420

    AlaAlaAlaProAlaArgArgGlnAlaArgAlaAlaAlaAlaAlaAlaThrArgAlaProPro 160
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    201    ProProAlaValAlaAlaArgGluProLeuProProProGlnProProf
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601    CCGCCCGGCCGTCGCCGCCCGGAGAGCCGCCGTGCCCGCCGCGCGCCACCAGCCGCCGGC

Qy    221    ProGlnGlnGlnProProProProGlnProProProGluProGlyGly?
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661    CCACAGCAGCAGCAGCCCGCCGCCGCCAGCCACAGCCGCCGCCGGGGGGGCG

Qy    241    ArgAlaGlyGlyAlaAlaArgProValSerSerLeuArgGluValValAlaArgTyrLeuG
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721    CGGGGCCGGCGGCGCGGCGCCCCCTGAGCCTGCGGGAAGTTCGTGCGTACCTCG

Qy    261    SerGlyGlyAlaGlyGlyTyrGlyArgLeuThrArgGlyValArgGlnGlyLeuLeuGluG
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781    AGCGGCGGGCCCGGCGGGTCGCCTAACCCCGCCGCCGGCCGCCGCCGTGCTGCTGGAGC

Qy    281    AlaAlaAlaArgGlyAlaGluArgGlyThrArgLeuGlyAlaLeuAlaLeuProA
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841    GCGGCGGCTCGAGGCCGTCTCGGACGGCGCACCCGTCTCGGAGGCTTGCGTGCCCC

Qy    301    AspArgProGlyArgGlyArgAlaProGlyAlaAlaSerAlaAlaArgProSerArgSerLysA
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901    GACAGGCCCCGACGGGCGCCGGCGCCGCGGGACCGCCCGCCGTCTCGCAGCAAGA

Qy    321    GlyGluGluArgValLeuGluLysGluGluGluGluGluAspAspAspGluAspGluA
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961    GGAGAAGAGCGGAGTACTTGAGAAAGAAGAAGAGGAAGGAAGGATGATGATGAAGATGAAAC

Qy    341    GluAspAspAlaSerGluGluGlySerGluValProGlySerGluAspArgProAlaGlyA
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021   GAAGATGATGTGTCAGAGGGCTCTGAGTGCCCGAGAGTGACCGTCCTGCAGTG

Qy    361    HisHisGlnLeuAsnGlyLysArgGlyProGlnSerAlaLysGluArgValLysG
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081   CACCACCAGCTTAACGGCGAGCGGGGACCTCAGAGTGCCAAGGAGAGGGTCAAGC

Qy    381    ThrProCysGlyProHisGlnGlyGlnGlnLysAspGluArgGlyLeuProGlyLys
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141   ACCCCCTGCGACCGCACCAGGCCAGGATGGAAGGCGGGGGCCAGCCCCCGGGCA

Qy    401    ThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyThrAlaServ
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201   ACCCCGCCAGGTGTTCTTCCATGGCAGCCATGAACAAGGAAGGGGAACAGCTTCTG

Qy    421    ThrGlyProAspSerProSerProValProLeuProProGlyTyrLysProAlaLeuP
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261   ACCGGGCCAGACTCCCCCGTCCCCGTGCCTTTGCCCCCAGGCAAACCAGCCCTAC

Qy    441    AlaAspGlyThrProPheGlyCysProProGlyArgLysGlyLysProSerAspP
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321   GCCGACGGGACCCCCTTTGGTCGTCCGGCCGGGCAAAGAAGGCCATCTGATC

Qy    461    GluTrpThrValMetAspValValGluTyrPheThrGlnAlaGlyPheProGluG
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381   GAGTGGACCGTGATCGAATGTCGTCGAATATTTTTACTGAGCGTGGATTCCCGGAGC

Qy    481    ThrAlaPheGlnGluGlnIleAspTyrLysSerLeuLeuMetGlnArgT
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441   ACAGCTTTCCAAGAGCAGGAAATTGATGGCAAATCTTTGCTGTCTCATGCAGCGCA

Qy    501    ValLeuThrGlyLeuSerIleArgGluGlyProAlaLeuLysIleTyrGluHisH
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501   GTGTCACCGGCCTGTCCATCCGCCTCGGAGCCCTGAAAATCTACGAGCACC.

Qy    521    LysValLeuGlnGlnGlyHisPheGluGlnAspProAspProGlyPheLeuGly
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561   AAGGTGCTTCAGCAAGGCCACTTTGAGGATGATGACCCCGATGGCGTTCTTAGGC
```

RESULT 4
US-10-023-523-45

```
pplication US/10023523
. US20020152485A1
ATION:
es, Ann M.
ees, Robert S.
aw, Simon W.
rjona, Anibal A.
NTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
NTION:  PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
NTION:  ATHEROSCLEROSIS
E: 10797-004001
CATION NUMBER: US/10/023,523
G DATE:  2001-12-17
TION NUMBER: US/09/616,289
DATE: 2000-07-14
TION NUMBER: US 09/517,849
DATE: 2000-03-02
TION NUMBER: US 08/979,608
DATE: 1997-11-26
TION NUMBER: US 60/031,930
DATE: 1996-11-27
TION NUMBER: US 60/048,547
DATE: 1997-06-03
 ID NOS: 53
tSEQ for Windows Version 4.0

mo sapiens

S
)...(1614)

:
           5.74e-144        Length:          1614
           2850.00          Matches:         538
cy:        100.00%          Conservative:    0
arity:     100.00%          Mismatches:      0
           100.00%          Indels:          0
           13               Gaps:            0

 (1-538) x US-10-023-523-45 (1-1614)

AlaGlyProProAlaLeuProProProGluThrAlaAlaAlaAlaThrThrAlaAla 20
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GCGGGGCCCCCGGCCCTACCCCCGCCGGAGACGGCGGCGGCCGCCACCACGGCGGCC 60

AlaSerSerSerAlaAlaSerProHisTyrGlnGluTrpIleLeuAspThrIleAsp 40
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GCCTCGTCGTCCGCCGCTTCCCCGCACTACCAAGAGTGGATCCTGGACACCATCGAC 120

LeuArgSerArgLysAlaArgProAspLeuGluArgIleCysArgMetValArgArg 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CTGCGCTCGCGCAAGGCGCGGCCGGACCTGGAGCGCATCTGCCGGATGGTGCGGCGG 180

HisGlyProGluProGluArgThrArgAlaGluLeuGluLysLeuIleGlnGlnArg 80
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CACGGCCCGGAGCCGGAGCGCACGCGCGCCGAGCTCGAGAAACTGATCCAGCAGCGC 240

ValLeuArgValSerTyrLysGlySerIleSerTyrArgAsnAlaAlaArgValGln 100
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GTGCTCCGGGTCAGCTACAAGGGGAGCATCTCGTACCGCAACGCGGCGCGCGTCCAG 300

ProArgArgGlyAlaThrProProAlaProProArgAlaProArgGlyAlaProAla 120
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CCCCGGCGCGGAGCCACCCCGCCGGCCCCGCCGCGCGCCCCCGCGGGGCCCCCGCC 360

AlaAlaAlaAlaAlaProProProThrProAlaProProProProProAlaProVal 140
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GCCGCCGCCGCCGCGCCGCCGCCCACGCCCGCCCCGCCGCCACCGCCCGCGCCCGTC 420

AlaAlaAlaProAlaArgAlaProArgAlaAlaAlaAlaAlaAlaThrAlaProPro 160
```

```
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 GCCGCCGCCGCCCCGGCCCGGGCGCCCCGCGCGGCCGCCGCCGCCGCCACAGC

Qy         161 SerProGlyProAlaGlnProGlyProArgAlaGlnArgAlaAlaProLeuAl
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 TCGCCTGGCCCCGCGCAGCCGGGCCCCCGCGCGCAGCGGGCCGCGCCCCTGGC

Qy         181 ProProAlaProAlaAlaProProAlaValAlaProProAlaGlyProArgAr
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 CCGCCCGCGCCAGCCGCTCCCCCGGCGGTGGCGCCCCCGGCCGGCCCGCGCCG

Qy         201 ProProAlaValAlaAlaArgGluProProLeuProProProProGlnProPr
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 CCGCCCGCCGTCGCCGCCCGGGAGCCGCCGCTGCCGCCGCCGCCACAGCCGCC

Qy         221 ProGlnGlnGlnGlnProProProProGlnProGlnProProProGluGlyGl
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 CCACAGCAGCAGCAGCCGCCGCCGCCGCAGCCACAGCCGCCGCCGGAGGGGG

Qy         241 ArgAlaGlyGlyAlaAlaArgProValSerLeuArgGluValValArgTyrLe
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 CGGGCCGGCGGCGCGGCGCGGCCCGTGAGCCTGCGGGAAGTCGTGCGCTACCT

Qy         261 SerGlyGlyAlaGlyGlyArgLeuThrArgGlyArgValGlnGlyLeuLeuGl
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 AGCGGCGGCGCCGGCGGTCGCCTAACCCGCGGCCGCGTGCAGGGGCTGCTGGA

Qy         281 AlaAlaAlaArgGlyArgLeuGluArgThrArgLeuGlyAlaLeuAlaLeuPr
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 GCGGCGGCTCGAGGCCGTCTGGAGCGCACCCGTCTCGGAGCGCTTGCGCTGCC

Qy         301 AspArgProGlyArgAlaProProAlaAlaSerAlaArgProSerArgSerLy
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 GACAGGCCCGGACGGGCGCCGCCGGCCGCCAGCGCCCGCCCGTCTCGCAGCAA

Qy         321 GlyGluGluArgValLeuGluLysGluGluGluGluAspAspAspGluAspGl
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 GGAGAAGAGCGAGTACTTGAGAAAGAAGAGGAAGAAGATGATGATGAAGATGA

Qy         341 GluAspAspValSerGluGlySerGluValProGluSerAspArgProAlaGly
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 GAAGATGATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCCTGCAGGT

Qy         361 HisHisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluArgValLys
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 CACCACCAGCTTAACGGCGAGCGGGGACCTCAGAGTGCCAAGGAGAGGGTCAAG

Qy         381 ThrProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGly
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1141 ACCCCCTGCGGACCGCACCAGGGCCAGGATGAAGGGCGGGGGCCAGCCCCGGGC

Qy         401 ThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSer
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1201 ACCCGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGAACAGCTTCT

Qy         421 ThrGlyProAspSerProSerProValProLeuProProGlyLysProAlaLeu
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1261 ACCGGGCCAGACTCCCCGTCCCCCGTGCCTTTGCCCCCAGGCAAACCAGCCCTA

Qy         441 AlaAspGlyThrProPheGlyCysProProGlyArgLysGluLysProSerAsp
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1321 GCCGACGGGACCCCCTTTGGCTGTCCGCCCGGGCGCAAAGAGAAGCCATCTGAT

Qy         461 GluTrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGlu
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1381 GAGTGGACCGTGATGGATGTCGTCGAATATTTTACTGAGGCTGGATTCCCGGAG

Qy         481 ThrAlaPheGlnGluGlnGluIleAspGlyLysSerLeuLeuLeuMetGlnArg
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1441 ACAGCTTTCCAAGAGCAGGAAATTGATGGCAAATCTTTGCTGCTCATGCAGCGC

Qy         501 ValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

CTCACCGGCCTGTCCATCCGCCTCGGGCAGCCCTGAAAATCTACGAGCACCACATC 1560

```
Qy  ValLeuGlnGlnGlyHisPheGluAspAspArgProAspGlyPheLeuGly  538
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    GTGCTTCAGCAAGGCCACTTTGAGGATGATGACCCCGATGGCTTCTTAGGC  1614
```

plication US/10616187
US2004001368A1

TION:
s, Ann M.
es, Robert S.
w, Simon W.
jona, Anibal A.
TION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TION: ATHEROSCLEROSIS
: 10797-004001
ATION NUMBER: US/10/616,187
DATE: 2003-07-09
ION NUMBER: US/09/616,289
ATE: 2000-07-14
ION NUMBER: US 09/517,849
ATE: 2000-03-02
ION NUMBER: US 08/979,608
ATE: 1997-11-26
ION NUMBER: US 60/031,930
ATE: 1996-11-27
ION NUMBER: US 60/048,547
ATE: 1997-06-03
ID NOS: 53
SEQ for Windows Version 4.0

sapiens

...(1614)

```
        5.74e-144    Length:        1614
        2850.00      Matches:        538
/:      100.00%      Conservative:     0
        100.00%      Mismatches:       0
city:   100.00%      Indels:           0
        15           Gaps:             0
```

(1-538) x US-10-616-187-45 (1-1614)

```
Qy  AlaGlyProProAlaLeuProProGluThrAlaAlaAlaAlaThrAlaAla  20
Db  BCGGGGCCCCCGGCCCTACCCCCGGCGGACGGCGGCCGCCACCACGGCGGCC

Qy  AlaSerSerAlaAlaSerProHisTyrGlnGluTrpIleLeuAspThrIleAsp  40
Db  BCCTCGTCGTCCGCCTCCCCCGCACTACCAAGAGTGGATCCTGGACACCATCGAC  120

Qy  LeuArgSerArgLysAlaArgProAspLeuGluArgIleCysArgMetValArgArg  60
Db  CTGCGTCGCGCAAGGCGCGGCCGGACCTGGAGCGCATCTGCCGGATGGTGCGGCGG  180

Qy  HisGlyProGluProGluArgThrArgAlaGluLeuGluLysLeuIleGlnGlnArg  80
Db  ACCGGCCCGGAGCCCGAGCGCACGCGCGCCGAGCTCGAGAAACTGATCCAGCAGCGC  240

Qy  ValLeuArgValSerThrTyrLysGlySerIleSerTyrArgAsnAlaAlaArgValGln 100
Db  GTGCTCCGGGTCAGCTACAAGGGGAGCATCTCGTACCGCAACGCGCGGCGTCCAG  300

Qy  ProArgArgGlyAlaThrProProAlaProProArgProArgGlyProArgGlyAlaProAla 120
```

```
3072  Db  GCCGTGCTCCGGGTCAGCTACAAGGGAGCATCTCGTACCGCAACGCGCGCCG
 101  Qy      ProProArgArgGlyAlaThrProAlaProProAlaProArgAlaProArgGlyAl
              |||||||||||||||||||||||||||||||||||||||||||||||||||
3132  Db      CCGCCCCGGCGGCGGAGCCACCCCCGGCCCGCCCGGCGCCCGCGCCCCGGGGGC
 121  Qy  AlaAlaAlaAlaAlaAlaProProThrProAlaProProProProProA
          ||||||||||||||||||||||||||||||||||||||||||||||||
3192  Db  GCCGCCGCCGCCGGCGCCCGCCCACGCCCCGCCCACCGCCGCCGC
 141  Qy  AlaAlaAlaAlaProAlaArgAlaProAlaArgAlaAlaAlaAlaAlaThrAl
          ||||||||||||||||||||||||||||||||||||||||||||||||
3252  Db  GCCGCCGCCGCCGCCCGGGCGCCCGGGCGCCCGGCGGGGGCCGCCGCCCACAGC
 161  Qy  SerProGlyProAlaGlnProGlyProArgAlaGlyAlaProLeuAl
          ||||||||||||||||||||||||||||||||||||||||||||||
3312  Db  TCGCCTGGCCCCGGCAGCCCGGGCCCCCGGCGCAGCGGAGCCCGGC
 181  Qy  ProProAlaProAlaAlaProProAlaValAlaProAlaGlyProArgAr
          ||||||||||||||||||||||||||||||||||||||||||||||
3372  Db  CCGCCCCGGCGCCCAGCGCCGCTCCCCGGCGGTGGCCCCCGGCGCCGGCCCG
 201  Qy  ProProAlaValAlaAlaArgGluProProLeuProProProGlnProProPr
          |||||||||||||||||||||||||||||||||||||||||||||||
3432  Db  CCGCCCCGTGCCCGCCCGGGAGCCGCGCCTGCCCGGCCGCCCGCCACAGCCGCC
 221  Qy  ProGlnProGlnProGlyProProProGlnProGlnProProProGluGlyGl
          |||||||||||||||||||||||||||||||||||||||||||||||
3492  Db  CCACAGCAGCAGCACGCCGCCGCCGCCGCCAGCCCGCCGGGAGGGGG
 241  Qy  ArgAlaGlyGlyAlaAlaAlaArgProValSerLeuArgGluValValAlaArgTyrLe
          ||||||||||||||||||||||||||||||||||||||||||||||
3552  Db  CGGGGCCGGCGCGCGCCGGCGCCCGTGAGCCTGGGGAAGTCGTGGCTACCT
 261  Qy  SerGlyAlaGlyGlyArgLeuThrArgGlyArgValGlnGlyLeuLeuGl
          ||||||||||||||||||||||||||||||||||||||||||||||
3612  Db  AGCCGGCGGCCGCGCGCCGGCCGTCGCCTAACCCGGCGCCCGGGCTGCTGAC
 281  Qy  AlaAlaAlaArgGlyArgLeuGlyArgThrArgLeuGlyAlaAlaLeuPrc
          |||||||||||||||||||||||||||||||||||||||||||||
3672  Db  GCGGCGGCTCGAGGCGGTCTTGGAGCGCAGCCACCCGGTCTCGGAGCGCTTGCGCTGCCC
 301  Qy  AspProArgProGlyArgAlaProAlaProAlaAlaSerAlaAlaArgProSerArg----
          |||||||||||||||||||||||||||||||
3732  Db  GACAGGCCCGGACGGGCGCCGGCGCCCCGGCGCCCCGTCTCGCAGCAAG
 316  Qy  -------------------------------------------
3792  Db  GCGCCGGGGAGGACGGGGGGCGGCGCCGGGTGGGCAGGTGCGGGCGAAGTTGGTGGC
 316  Qy  -------------------------------------------
3852  Db  GCGAGTCCCGGAGGAACTGGGTGGCGGGTGGCGTGGCGGCTTGGGGCGCGTTTCC
 316  Qy  -------------------------------------------
3912  Db  CTCGGTGGTGGTGACCTTGGCAAGTGTTGGCAAGTGATGATTGAATCTCCCGGAGCCTCAGTTTCC
 316  Qy  -------------------------------------------
3972  Db  GTAAACGCGGTTTAATAACAGTAGCGACCCCTTGGGGTTGTTGAGCGAGTTTAG
 316  Qy  -------------------------------------------
4032  Db  TTGGTTGTCGAGGGCTTTAGTTAACACAGAGCCTGGCACGGAGTGAATGCGTAAA
 316  Qy  -------------------------------------------
4092  Db  GTCCGTATTGTTCTTAAAGGTGGAATCGGTTCCTCCTCCCCACCGCCCGGACGC
 317  Qy  --------------------------------------Ser
                                                    |||
4152  Db  CAGGGTCTGGGATTAGAACAGCTACTAATTTGCATGCTTCTCTCCTCGGGCTCA
```

```
GTGACCGTGATGAGTGTCTGCGAATATTTACTGAGGCTGGATTCCCGGAGCAGGCG   1440  Db
ArgAlaPheGlnGluGlnGlnIleAspIleGlySerLeuLeuMetGlnArgThrAsp   500  Qy
|||||||||||||||||||||||||||||||||||||||||||||||||||||||
AGCTTCCAAGAGACGAGGAAATTGATGGCAAATCTTTGCTGCTCCATGCAGCGCACAGAT  1500  Db
IleLeuThrArgGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIle   520  Qy
|||||||||||||||||||||||||||||||||||||||||||||||||||||
GCTCACCGGCCTGTCCATCCGCTCGGGCCCAGCCCTGAAAATCTACGAGCACCACCATC  1560  Db
ValLeuGlnGlnGlyHisPheGluGlnGlyHisAspAspAspProAspGlyPheLeuGly   538  Qy
|||||||||||||||||||||||||||||||||||||||||||||
GGTGCTTCAGCAAGGCCACTTTGAGGATGATGACCCCGATGGCTTCTTAGGC  1614  Db
```

tSEQ for Windows Version 4.0

5

no sapiens

```
:        6.82e-131     Length:      12425
         2616.50       Matches:       536
y:       69.16%        Conservative:    0
rity:    69.16%        Mismatches:      2
         91.81%        Indels:        239
         9             Gaps:            4
```

(1-538) x US-09-976-740-50 (1-12425)

```
AlaGlyProAlaLeuProProGluThrAlaAlaAlaAlaThrThrAlaAlaAla   20
|||||||||||||||||||||||||||||||||||||||||||||||
GCGGGGCCCCCGGCCCTACCCCCCGCCGGAGACGGGCGGCGCCGCCACCACGGCGGCC  2891
AlaSerSerSerAlaAlaSerProHisTyrGlnGluTrpIleLeuLeuAspThrIleAsp   40
||||||||||||||||||||||||||||||||||||||||||||||
GCCTCGTCGTCCGCCGCTTCCCCGCACTACCAAGAGTGGATCCTGGAACCATCGAC  2951
LeuArgSerArgLysAlaArgProAspLeuArgIleCysArgMetValArgArg   60
|||||||||||||||||||||||||||||||||||||||||||||||
CTGCGCCTCCGCAAGGCGCGGCCCGGACCTGAGCCATCTGCCCGATGTGCGGCGG  3011
HisGlyProGluProGlyThrArgAlaGluLeuGluLysGlnGlnArg   80
||||||||||||||||||||||||||||||||||||||||||||||
CACGGCCCCGAGCCGGGCACGCGCGCGGAGCTGGAGAAACTGATCCAGCAGCGC  3071
ValLeuArgValSerThrTyrLysGlySerIleSerArgTyrArgAsnAlaAlaArgValGln   100
|||||||||||||||||||||||||||||||||||||||||||||||
```

; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREA
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/671,242
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 12425
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-671-242-50

Alignment Scores:
Pred. No.:   Length: 12425
Score: 6.82e-131   Matches: 536
Percent Similarity: 2616.50   Conservative: 0
Best Local Similarity: 69.16%   Mismatches: 2
Query Match: 69.16%   Indels: 239
DB: 91.81%   Gaps: 4
                      12

US-09-976-740-43 (1-538) x US-10-671-242-50 (1-12425)

Qy   1 MetAlaGlyProProAlaLeuProProGluThrAlaAlaAlaAlaThrA
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2832 ATGGCGGGGCCCCCCGCCCTACCCCCGCCGGACAGGCGGCCGCCACCACGG

Qy   21 AlaAlaSerSerAlaAlaSerProHisTyrGlnGluTrpIleLeuAspThrI
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2892 GCCGCCCTCGTCTGCTCCGCGCTTCCCCGCACTACCAAGAGTGGATCCTGGACACCA

Qy   41 SerLeuArgSerArgLysAlaArgProAspLeuGluArgIleCysArgMetValA
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2952 TCGCTGCGCTCGCGCAAGGCGCGGCCGGACCTGGAGCGCATCTGCCGGATGGTGG

Qy   61 ArgHisGlyProGluArgThrArgAlaGluLeuGluLysLeuIleGlnG
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3012 CGGCAGCCCGGGGAGCGCCGGAGCCGGAGGCGACCGCGGCCGAGCTCGAGAACTGATCCAGC

Qy   81 AlaValLeuArgValSerTyrLysGlySerIleSerTyrArgAsnAlaAlaArgVa
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3072 GCCGTGCTCCGGGTCAGCTACAAGGGGAGCATCTCGTACCGCAACGCGGCGCGCGT

Qy   101 ProProArgArgGlyAlaThrProProAlaProArgAlaProAlaGlyAlaProP
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3132 CCGCCCGCGCGCGGCGGAGCCACCCCGCCGCCCCCGCGGGCCCCGGGGGGCCCC

Qy   121 AlaAlaAlaAlaAlaAlaProProProThrProProAlaProProProProAlaPr
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3192 GCCGGCCGCCGCGCGCCGCCGGCGCCCCCACGCCCGCCACCGCCCCGGCGCC

Qy   141 AlaAlaAlaAlaProAlaAlaArgAlaProArgAlaArgAlaAlaAlaAlaThrAlaPr
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3252 GCCGCCCGCGCCCCCGGCGCCCCGGCCGCGCGCGGCCGGGCGCCCCACCAGCGCC

Qy   161 SerProGlyProGlnProGlyProArgAlaGlnArgAlaAlaAlaProLeuAlaAl
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3312 TCGCCTGGCGCCCCCGCGCAGCCGGGCCCCGCGCGCGCAGCCGGCCGCGCCCTGGCCGC

Qy   181 ProProAlaProAlaAlaProAlaValAlaProAlaProAlaGlyTyrProAlaArgArgGlyA

GCCCGCGCCGCGCTCCCCCGGCGCCGGCCCCGGCGCGGCCGCCGCCCCC 3431

oProAlaValAlaAlaArgGluProProLeuProProGlnProProAlaPro 220
|||||||||||||||||||||||||||||||||||||||||||||||
GCCCCGCCGTGCCGCCCCGGGAGCCGCCGCTGCCCGCGCCGGCCACCAGCCGCCGGCCG 3491

oGlnGlnGlnGlnProProProProGlnProGlnProGluGlyGlyAlaVal 240
|||||||||||||||||||||||||||||||||||||||||||||||
ACAGCAGCAGCAGCCGCCGCCCCGCCCGCCGCCAGCCGCCGCCGGAGGGGGCGGGGTG 3551

gAlaGlyGlyGlyAlaAlaAlaArgProValSerLeuArgGluValValArgTyrLeuGlyGly 260
|||||||||||||||||||||||||||||||||||||||||||||||
GGCGGCGGCGGCGGCGGCGGCCGTGAGCCTGCGGGAAGTCGTGCGCTACCTCGGGGGC 3611

rGlyGlyAlaGlyGlyAlaArgLeuThrArgGlyArgValGlnGlyLeuLeuGlnGluGlu 280
|||||||||||||||||||||||||||||||||||||||||||||||
CGGCGGCGGCCGGCGGGTCGCTCACCCGCGGCCGCGTGCAGGGGCTGCTGCAGGAGGAG 3671

aAlaAlaArgGlyArgGluArgThrArgLeuLeuLeuAlaLeuProArgGly 300
|||||||||||||||||||||||||||||||||||||||||||||||
GGCGGCTCGAGGCGCGTCTCGAGCGCCACCCGTCTCGGAGACGCTTCGGAGACGCTGCCCGCGGG 3731

pArgProGlyAlaProProAlaAlaSerAlaArgProSerArg---------- 316
|||||||||||||||||||||||||||||||||||||
CAGGCCCGGACGGGCCGCCCGCCCGCCCCGCTCTCGCAGCAAGGTGAGC 3791

-- 316

3CCGGGGAGCCGGGGGCGCCGCGGCGGTGGCAGGTGCGGCGAAGTGGTGGCGGGGGC 3851

-- 316

3AGTCCCGGAGGAACTGGGTGGCGGGTGGCTTTGCGCGGCGTTTCCTGCGGG 3911

SerLysArg 319
||| |||
GGTCTGGGATTAGAACAGCTACTAATTTTGCATGCTTCTCTCCTCCGGCTCCAG-AGA 4210

GlyGluGluArgValLeuGluLysGlnGluGluGluGluLysGluAspAspArgGluAspGluAsp 339
|||||||||||||||||||||||||||||||||||||||||||||||
GGAGAGGAGCGAGTACTTGAGAAAGAGAGAAGAAGATGATGAAGATGAAGAT 4270

GluAspAspValSerGluGlyLySerGluValProGluSerAspArgProAlaGlyAla 359
|||||||||||||||||||||||||||||||||||||||||||||||
GAAGATGATGTGTCAGAGGGTTCTGAAGTGCCCGAGAGTGACCGTCCTGCAGGTGCC 4330

HisHisGlnLeuAsnGlyGlyArgGlyProGlnSerAlaLysGlyValLysGlu 379
|||||||||||||||||||||||||||||||||||||||||||||||
CACCACCAGCTTAACGGCGGACGGGGACCTCAGAGTGCCAAGGAGGGTCAAGGAG 4390

ThrProCysGlyTyrProHisGlnGlyGlnAspGluArgGlyArgProAlaProGlySer 399
|||||||||||||||||||||||||||||||||||||||||||||||
ACCCCCTGCGGACACCGACCCAGGATGAAGGGCGGGGCCAGCCCCCGGGCAGC 4450

ThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyThr---------- 416
||||||||||||||||||||||||||||||||||||
ACCCGGCCAGGTGTTCTCATGGCAGCCATGAACAAGGAAGGGGGACAGGTAAGGAT 4510

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416 --

Qy

Db 4511 CCCTCTGGTGGGGAAGAGTGCTAGGTGGAGAGGAACTCAGCCGAGAGACAA

417 ----------AlaSerValAlaThrGlyProAspSerProS

Qy

Db 4571 ACAGGTGTTTTTTCCTTCCCAGCTTCTGTTGCCACCGGGCCAGACTCCCGT

429 lProLeuProProGlyGlyLysProAlaLeuProGlyAlaAspGlyThrProPheG

Qy

Db 4631 GCCTTTGCCCCCAGGCAAACCAGCCCTACCTGGGGCCGACGGGACCCCCTTTG

449 o---

Qy

Db 4691 GTAAGTTGGGGTATTGGAGACATGGGGGTGCTGCTCAGGTGTGTGGTACAGCCJ

450 --ProGlyArgGlyLysGlu

Qy

Db 4751 CATCCGTGTTCACTGGTGTCTGTTTTGTTTTGATGCAGTCCCGGGCCAAAGAGA

457 erAspProValGluTrpThrValMetAspValValGluTyrPheThrGluAlaAc

Qy

Db 4811 CTGATCCCGTGGAGTGGACCGTGATGGATGTCGTCGAGCAAGGTGAGCTC

477 roGluGlnAlaThrAlaPheGlnGlu----------

Qy

Db 4871 CGGAGCAGGCGCACAGCTTTCCAAGA-GCAGGTGAGTTTCCAGCCCAGGACTACA

485 --

Qy

Db 4930 CAGACACAGAGGGCCCTCCCTGGGATGTGCCCGATCCCGGCCTTCTCTGTTCCT

486 --GlnGluIleAspGlyLysSerLeuLeuMetGlnArgThrAspValLeuT

Qy

Db 4990 CCCAGGAAATTGATGGCAAATCTTTGCTGCTCATGCAGCGGCACAGATGTGCTCA

505 euSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisIleLysVall

Qy

Db 5050 TGTCCATCCGCCTCGGGCCCAGCCCTGAAAATCTACGAGCACCATCAAGGTGC

525 lnGlyHisPheGluAspAspAspProAspGlyPheLeuGly 538

Qy

Db 5110 AAGGCCACTTTGAGGATGATGACCCCGATGGCTTCTTAGGC 5150

RESULT 8
US-10-023-529-50
; Sequence 50, Application US/10023529
; Publication No. US20020129388A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREI
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/023,529
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 50

o sapiens

```
         6.82e-131    Length:        12425
         2616.50      Matches:         536
y:       69.16%       Conservative:      0
rity:    69.16%       Mismatches:        2
         91.81%       Indels:          239
         13           Gaps:              4
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(1-538) x US-10-023-529-50 (1-12425)

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AlaGlyProProAlaLeuProProProGluThrArgAlaAlaAlaAlaThrThrAlaAla  20
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GCGGGGCCCCCGGAGACGGCGGCGGCCCGGGAGACGGCGGCGGCCCCACCACCGCGGCC  2891
```

```
AlaSerSerAlaAlaSerProHisTyrArgGlnGluTrpIleLeuAspThrIleAsp  40
|||||||||||||||||||||||||||||||||||||||||||||||||||||
GCCTCGTCTCGCCGCTTCCCCGCACTACCAAGAGTGGATCCTGGACACCATCGAC  2951
```

```
LeuArgSerArgLysAlaArgProAspLeuGluArgIleCysArgMetValArgArg  60
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CTGCGGTCGCGCAAGGCGCGGGACCTGGAGCGCATCTGCCGGATGGTGCGGCCG  3011
```

```
HisGlyProGluProGluThrArgAlaGluLeuGlyLysLeuLeuGlnGlnArg  80
||||||||||||||||||||||||||||||||||||||||||||||||||||||
CACGGGCCGGAGCCGGAGACGCGCGCAGCTCGAGAAACTGAATCCAGCAGCGC  3071
```

```
ValLeuArgValSerTyrLysGlySerIleSerTyrArgAsnAlaAlaArgValGln  100
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GTGCTCCGGGTCAGCTACAAGGGAGCATCTCGTACCGCAACGCGGCGCGGGTCCAG  3131
```

```
ProArgArgGlyAlaThrProProProAlaProAlaProArgGlyAlaProAlaPro  120
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CCCCGGCGCGGAGCCACCCCGCCCCCGGGCCCCCGCGCCGGGGGCCCCCGGCCCCG  3191
```

```
AlaAlaAlaAlaAlaProProThrProAlaProProProProAlaProAlaProVal  140
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GCCGGCCGCCGGCCGCCGCCGCCACGCCCCGCCCCCGCCGCCCCACCGCCCCCGTC  3251
```

```
AlaAlaAlaAlaProAlaArgArgAlaProAlaAlaAlaAlaAlaAlaThrAlaPro  160
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GCCGGCCGCCGCGGCCCCGGGCGCCCCGGGCGCCCCGGCGCCGCCACAGCGCCCCC  3311
```

```
ProGlyProAlaGlnProGlyProAlaArgGlnAlaProArgLeuAlaProAlaPro  180
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CCTGGCCCCGCGCAGCCCGGGCCCCGGCCGCCAGGCCCCGCGCCTGGCCGCGCCG  3371
```

```
ProAlaProAlaAlaProAlaValAlaProProAlaProAlaGlyProAlaProAla  200
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CCCGCGCCAGCGCTCCCCCGGGTGGCGCCCCCGGCCCCGCGCCGGGCCCGCGCCCC  3431
```

```
ProAlaValAlaAlaAlaArgGluProLeuProProGlnProProGlnProAlaPro  220
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CCGGCCGTTCGCGCCGCGGAGCCGCTGCCGCCCCAGCCGCCGCAGCCCGGGCCG  3491
```

```
GlnGlnGlnProProProGlnProProGluGlyValGlyAlaVal  240
||||||||||||||||||||||||||||||||||||||||||||||
AGCAGCAGCAGCCGCCGCCGCAGCCGCCACAGCCAGCGGGGGCGGGTG  3551
```

```
AlaGlyGlyAlaAlaAlaArgProValSerLeuArgGluValArgTyrLeuGlyGly  260
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GCCGGCGGCGCGGCGGCGCGGCCCGTGAGCCTGCGGGAAGTCCGGTACCTGGGGGGC  3611
```

```
GlyGlyAlaGlyGlyValArgLeuThrArgGlyValArgGlnValLeuLeuGluGlu  280
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GCGCGGCGCCGGCGGTCGCCTAACCCGGCGGCCGTGCAGGGGCGTGCTGCAGGAGGAG  3671
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AlaAlaAlaGlyArgThrArgLeuGluLeuGlyAlaLeuAlaLeuAlaLeuProArgGly  300
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GCGCGGCGCCGGCGGTCACT...
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```
Db  3672  GCGGCCGGCTCGAGGCGCCGTCTCGGAGCGCCACCGTCTCGGAGGCGCTTGCGCTGCCCC
Qy   301  AspArgProGlyArgGlyArgAlaProProAlaAlaSerAlaAlaArgProSerArg
                                                              ---------
Db  3732  GACAGGCCCCGACGGCGCGGGCGCCCGGCGGCGCCGAGCGCCCGCGTCTCGCAGCAAGC
Qy   316  ---------------------------------------
Db  3792  GCGCCCGGGGAGCGGGGCGCGCCGCGGTGGGCAGTGCGGGCGAAGTTGGTGGCC
Qy   316  ---------------------------------------
Db  3852  GCGAGTCCCGGGAGGAACTGGGTGGCCGGTGCTGGGGCTTTGCGCGCGTTTCCT
Qy   316  ---------------------------------------
Db  3912  CTCGGTGCGTGGTGACCTTGGCAAGTGATTGATTGAATCTCCCGAGCCTCAGTTTCCT
Qy   316  ---------------------------------------
Db  3972  GTAAACGCGGTTAATAACAGTAGCGACCCCTTGGGGTTGTTGAGCGAGTTTAGT
Qy   316  ---------------------------------------
Db  4032  TTGGTGTCGAGGGCTTAGTTAACACAGAGCCTGCACGAGTGAATGCGTAAA
Qy   316  ---------------------------------------
Db  4092  GTCCGTATTGTTCTTAAAGGTGGAATCGGTTCCTCCTCCCACCGCCCGAGACGCC
Qy   317                                          ------SerL
                                                        |||
Db  4152  CAGGGTCTGGGATTAGAACAGTACTACTAATTTGCATGCTTCTCTCCTCGGCTCCA
Qy   320  GlyGlyGlyGluGluLysGluLeuGluLysGluGluGluLysAspAspAspGluAspG
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4211  GGTGGAAGAGAGCGAGTACTTGAGAAAGAAGAGGAAGAAGATGATGATGAAGATG
Qy   340  GluGluAspAspValSerGluGlySerGluValProGluSerAspArgProAlaG
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4271  GAAGAAGATGATGTCAGAGGGCTCTGAAGTGCCCGAGAGTGCAGTCCTGCAG
Qy   360  GlnHisHisGlnLeuAsnGlyGluArgGluArgGlyProGlnSerAlaLysGluArgValL
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4331  CAGCACCACCAGCTTAACGGCAGCCGGGACCTCAGAGTGCCAAGGAGAGGGTCA
Qy   380  TrpThrProCysGlyProHisGlnGlyGlnAspGlyGluGlyArgGlyProAlaProG
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4391  TGGACCCCTGCGGACCGCACCAGGGCCCACGATGAAGGGCGGGGGCCCAGCCCCGG
Qy   400  GlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThr-----
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||---
Db  4451  GGCACCCGGCCAGGTGTTCTCCATGGCAGCCATGAACAACAGGAAGAGGGGGACCAGGTA
Qy   416  ---------------------------------------
Db  4511  CCCTCTGGGTGGGGAAGAGTGCTAGGTGGAGGAGGAACTCAGCCCGAAGACAAAGC
Qy   417  ------------AlaSerValAlaThrGlyProAspSerProSer
                        ||||||||||||||||||||||||||||||||
Db  4571  ACAGGTGTTTTTTCCTTCCCAGCTTCGTTGCCACCGGGCCAGACTCCCCGTCC
Qy   429  lProLeuProProGlyProLysProAlaLeuProArgGlyAlaAspGlyThrProPheGly
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4631  GCCTTTGCCCCCAGCCAAACCAGCCCTACCTGGGGCCACGGGACCCCCTTTGGC
Qy   449  o------------------------------------
Db  4691  GTAAGTTGGGGTATTGGAGACATGGGGTGCTGCTCAGGTGTGTGGTACCAGCAG
Qy   450  --------------------ProGlyArgLysGluLy
                                        |||
Db  4751  CATCCGTGTTCACTGGTGCTCGTTTGTTTGATGCAGTCCGGGCGCAAAGAGAC
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```
Db  2892  GCCGCCTCGTCGTCCGCCGCTTCCCCGCACTACCAAGAGTGGATCCTGGACAC
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    41  SerLeuArgSerArgLyeAlaArgProAspLeuGluArgIleCysArgMetVa
           
Db  2952  TCGCTGCGCTGCGCAAGGCGCCGGACCTGGAGCGCATCTGCCGGATGGT

Qy    61  ArgHisGlyProGluProGluArgThrArgAlaGluLeuGluLysLeuIleGl
           
Db  3012  CGGCACGGCCCGGAGACCCGAGCGCACGCGCCGAGCTGGAGAAACTGATCCA

Qy    81  AlaValLeuArgValSerTyrLysGlySerIleSerTyrArgAsnAlaAAr
           
Db  3072  GCCGTGCTCAGCTACACAAGGGGAGCATCTGTACCGCAACGCGGCGCG

Qy   101  ProProArgArgGlyAlaThrProProAlaProProArgAlaProArgGlyAl
           
Db  3132  CCGCCCCGGCGCGGGAGCCACCCCGGCGCCCCGGCGCGCCCCGCGGGGC

Qy   121  AlaAlaAlaAlaAlaAlaAlaProProProThrProAlaProProProAl
           
Db  3192  GCCGGCGCCGCCGCCGCGGCGCCACGCCCCACGCCCCGGCGCCCACCCCCGG

Qy   141  AlaAlaAlaAlaProAlaProAlaArgAlaProAlaArgAlaAlaAlaThrAl
           
Db  3252  GCCGGCCGCCGCCCGCCGGCGGCCCGGCGCCGCCGGCCGCCGCCACCAGC

Qy   161  SerProGlyProAlaGlnProGlyProArgAlaGlnArgAlaAlaProLeuAl
           
Db  3312  TCGCCCTGGCCCCCGGCAGCCGGCCCCCGGCGGGCCCCCGCCGCCGCCCTGGC

Qy   181  ProProAlaProAlaAlaAlaProProAlaValAlaAlaProProAlaGlyProAlaArc
           
Db  3372  CCGCCCCGGCGCCAGCGCCTCCCCGGCGGTGGCGCCCCGGCCGGCCCGGCGCCG

Qy   201  ProProAlaValAlaAlaArgGluProProLeuProProProGlnProPrc
           
Db  3432  CCGCCCGTGCCGCCCGGGAGCCCGCTCCCGCCGCCGCCCCAGCCGCCC

Qy   221  ProGlnGlnGlnProProProGlnProGlnInProGlnProGluProGlyG1y
           
Db  3492  CCACAGCAGCAGCAGCCGCCGCCCCGCCGCAGCCGCCGCCGGAGGGGGGC

Qy   241  ArgAlaGlyGlyGlyAlaAlaArgProValSerLeuArgGluValValArgTyrLeu
           
Db  3552  CGGGCCGGGGGAGGCGGGGCGGCCCGAGCCTGCGGGAAGTGGTGCGCTACCTC

Qy   261  SerGlyGlyAlaGlyGlyArgGlyArgValGlyArgValGlnGlyLeuLeuGlu
           
Db  3612  AGCGGCGGGGCCGGGGGTCGCTAACCCGGCGGCCGTGCAGGGGCTGCTGGAG

Qy   281  AlaAlaAlaArgGlyArgGluGluGlyLeuGluArgGlyLeuGlyAlaLeuAlaLeuPro
           
Db  3672  GCGGCGGCTCGAGGCCGTCGTCGAGCGCGCACCCGTCTCGAGCGCGTTGCGCTGCCC

Qy   301  AspArgProGlyArgGlyAlaProAlaAlaSerAlaArgProSerArg-------
           
Db  3732  GACAGGCCCGACGGGGCCCCGGCGGCCCCGTCTCGCAGCAAGC

Qy   316  ---------
Db  3792  GCGGCCGGGGAGGCGGGGCGCCGCGGTGGGCAGGTGCGGCGAAGTTGGTGGC

Qy   316  ---------
Db  3852  GCGAGTCCGGGAGGAGGAACTGGGGTGGCGGTGGTGGGCTTTGCGCGGTTC

Qy   316  -------
Db  3912  CTCGGGTGCGTGGTGACCTTGGCAAGTGATTGAATCTCCGGAGCCTCAGTTC

Qy   316  -------
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rAspProValGluTrpThrValMetAspValValGluTyrPheThrGluAlaGlyP  477
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TGATCCCGTCGAGTGGACCGTGATGATGTGTCGTCGAATATTTTACTGAGGCTGGATTCC  4870

gGluGlnAlaThrAlaPheGlnGlu--------------  485
GGAGCAGGCGACAGCTTTCCAAGA-GCAGGTGAGTTTCCAGCCCAGGACTACACACTGA  4929

--------  485
AGACACAGAGAGGGCCTTCCCTGGGATGTGCCCTGATCCGGCTTTCTCGTTCCTGTCCCA  4989

-GlnGlu1leAspGlyGlyLysSerLeuLeuLeuLeuMetGlnArgThrAspValLeuThrGlyL  505
CAGGAAATTGATGGCAAATCTTTGCTCATGCAGCGCACAGATGTGCTCACCGGCC  5049

uSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisIleLysValLeuGlnG  525
TCCATCCGCCTCGGGCCAGCCCTGAAAATCTACGAGCACCACATCAAGGTGCTTCAGC  5109

GlyHisPheGluAspAspProAspProPheLeuGly  538
GGCCACTTTGAGGATGATGACCCCGATGGCTTCTTAGGC  5150
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pplication US/10023523
.US20020152485A1
ATION:
es, Ann M.
ees, Robert S.
aw, Simon W.
rjona, Anibal A.
NTION:  NOVEL LOW DENSITY LIPOPROTEIN BINDING
NTION:  PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
NTION:  ATHEROSCLEROSIS
E: 10797-004001
CATION NUMBER: US/10/023,523
G DATE:  2001-12-17
TION NUMBER: US/09/616,289
DATE:  2000-07-14
TION NUMBER: US 09/517,849
DATE:  2000-03-02
TION NUMBER: US 08/979,608
DATE:  1997-11-26
TION NUMBER: US 60/031,930
DATE:  1996-11-27
TION NUMBER: US 60/048,547
DATE:  1997-06-03
ID NOS: 53
SEQ for Windows Version 4.0
```

```
no sapiens

          6.82e-131      Length:        12425
          2616.50        Matches:       536
y:        69.16%         Conservative:  0
rity:     69.16%         Mismatches:    2
          91.81%         Indels:        239
          13             Gaps:          4

(1-538) x US-10-023-523-50 (1-12425)
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AlaGlyProProAlaLeuProProGluThrProAlaAlaAlaAlaThrThrAlaAla  20
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GCGGGGCCCCCGGCCCTACCCCCGCCGGCGGCGACCGGCGGCCGGCCGCCACCGGCGGCC  2891

AlaSerSerSerAlaAlaSerProHisTyrGlnGluTrpIleLeuAspThrIleAsp  40
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Qy    525  lnGlyHisPheGluAspAspAspProAspGlyPheLeuGly 538
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Db   5110  AAGGCCACTTTGAGGATGATGACCCCGATGGCTTCTTAGGC 5150
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RESULT 10
US-10-616-187-50
; Sequence 50, Application US/10616187
; Publication No.US2004013668A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TRE.
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/616,187
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 50
;   LENGTH: 12425
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-616-187-50

Alignment Scores:
Pred. No.:   6.82e-131   Length: 12425
Score: 2616.50   Matches: 536
Percent Similarity: 69.16%   Conservative: 0
Best Local Similarity: 69.16%   Mismatches: 2
Query Match: 91.81%   Indels: 239
DB: 15   Gaps: 4

US-09-976-740-43 (1-538) x US-10-616-187-50 (1-12425)

Qy   1 MetAlaGlyProProAlaLeuProProGluThrAlaAlaAlaAlaThrThrA
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Db   2832 ATGGCGGGGCCCCCGGCCCTACCCCGCCCGGAGACGGCGCCGGCCGCCACCACGG

Qy   21 AlaAlaSerSerAlaAlaSerProHisTyrGlnGluTrpIleLeuAspThrI
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2892 GCCGCCTCGTCGTCGCCGTTCCCCGCCACTACCAAGAGTGGATCCTGGACACCA

Qy   41 SerLeuArgSerArgLysAlaAlaProLeuAspLeuCysArgMetValA
               ||||||||||||||||||||||||||||||||||||||||||||||||
Db   2952 TCGCTGCGCTCGCGCAAGGCGCCGCCGCTGGACCTGTGCCGGATGGTGC

Qy   61 ArgHisGlyProGluProGluArgThrArgAlaThrArgAlaGluLysLeuIleLeuGlnG
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3012 CGGCACGGCCCGGAGCCGGAGCGCACGCGCGCGACTCGAGAAACTGATCCAGCA

Qy   81 AlaValLeuArgValSerTyrLysGlySerIleSerTyrArgAsnAlaAlaArgVa
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3072 GCCGTGCTCCGGGTCAGCTACAAGGGGAGCATCTCGTACCGCAACGCGGCGCGCGT

Qy   101 ProProArgArgGlyAlaThrProAlaProAlaProArgAlaProArgGlyAlaPr
               ||||||||||||||||||||||||||||||||||||||||||||||||
Db   3132 CCGCCCCGGCGGGGAGCCACCCCGCCCGCCCCGCCCGGGCCCGCCCCCGGGGGCCCC

Qy   121 AlaAlaAlaAlaAlaAlaAlaAlaProProProThrProAlaProAlaProProProAlaPr
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(left column sequences, top to bottom)

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AAACGGGGTTTAATAACAGTAGCGACCCCCTTGGGGTTGTTGAGCGAGTTTAGTAAGAT 4031
-------------------------------------------------------------- 316
GGTTGTCGAGGGCTTTAGTTAACACAGAGCTGGCACGCGGAGTGAATGCGTAAAAGTTA 4091
-------------------------------------------------------------- 316
CGTATTGTTCTTAAAGGTGGAATCGGTTCCTCTCCCCACGCCCCGGACGCCACAGT 4151
                                                   SerLysArg 319
                                                     ||  ||
GGGTCTGGGATTAGAACAGCTACTAATTTGCATGCTTCTCTCCTCGGCTCCAG-AGA 4210
GlyGluGluArgValLeuGluLysGluGluGluGluGluAspAspAspGluGluAsp 339
GGGAGAAGCCGAGTACTTGAGAAAGAGAAGAAGAGGAAGAGAGAGATGATGATGAAGAAGAT 4270

GluAspAspValSerGlyGlySerGluValProGluSerGluAspArgProAlaGlyAla 359
GAAGATGATGTGTCAGAGGGCTCTGAAGTGCCCCAGAGTGACCGTCCTGCAGGTGCC 4330
HisHisGlnLeuAsnGlyHisGluArgGlyTyrProGlnSerArgAlaLysGluArgValValLysGlu 379
CACCACCAGCTTAACGGACGGCGGAGCCGGGACCTCAGATGCCAAGGAGGAGGGGTCAAGGAG 4390
ThrProCysGlyTyrProHisSerGlnGlyGlnAspGlyGlnAspArgGlyTyrArgGlyTyrProAlaProGlyTyrSer 399
ACCCCCTGCGGACCGCCACCAGGGCCAGGATGAGAGGGCCGGAGGGGCCAGCCCGGGCCAGC 4450
ThrArgGlnValPheSerMetAlaAlaAlaMetAlaAlaAsnLysGlyGlyTyrThr-------- 416
ACCCGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGAACAGGTAAGGAT 4510
-------------------------------------------------------------- 416
TCTGGGTGGGGAAGAGTGCTAGGTGGAGAGGAACTCAGCCCCGAAGACAAAGCCAAAG 4570
------------AlaSerValAlaThrGlyProAspProSerProSerProVa 429
GGTGTGTTTTTTTCCTTCCCCAGCTTCTCGTTGTTGCCACCGGGCCCAGACTCCCCGTCCCCGT 4630
GLeuProProGlyLysProProGlyProAlaAlaLeuProGlyTyrAlaAspGlyThrProPheGlyCysProPr 449
GCTTGCCCCCAGGCAAACCAGCCCCTACCTGGGGCCGACGGGACCCCCCTTTGGCTGTCC 4690
-------------------------------------------------------------- 449
AGTTGGGGTATTGGACACATCGGGGGTGCTCGTCTCAGGTGTGTACAGCGCAGAGAGA 4750
--------------------------ProGlyArgLysGluLysProS 457
CGGTGTTCACTGTGTCGTGTTTTGTTTTGATGCAGTCCCGGGCGCAAAGAGAGAAGCCAT 4810
ApProValGluTrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheP 477
GTCCCGTCAGTGACCGTGATGGATGTCGTCGAATATTTTACTGAGGCTGGATTCC 4870
uGlnAlaThrAlaPheGlnGlu------ 485
GCAGGCGACAGCTTTCCAAGA-GCAGGTGAGTTTCCAGCCCAGACTACACACTGA 4929
-------------------------------------------------------------- 485
CACAGAGGGCCTCCCTGGGATGTGCCCTGATCCCGGCGTTTCTCGTTCCTGTCCCA 4989
nGluIleAspGlyLysLysSerLeuLeuLeuMetGlnArgThrAspValLeuThrGlyLyL 505
GCCGTGCTCCCGGGTCAGCTACAAGGGGAGCATCTCGTACCAGTGCTCACCGGCC 5049
rIleArgLeuGlyProAlaLeuHisLysTyrGlyLuHisHisIleLysHisValLeuGlnG 525
CATCCGCCTCCGGGCCAGCCCTGAAAATCTACGAGCACCACCATCAAGGTGCTTCAGC 5109
AlaAlaAlaAlaAlaAlaAlaAlaAlaAlaProProProThrProAlaProAlaProProProAlaPr
```

Qy   4271 GAAGAAGAGATGATGTGTCAGAGGGTCTCGAGTGCCGAGAGTGACCGTCTGC
Db

Qy   360 GlnHisHisGlnLeuAsnGlyGluArgGlyGluProGlnSerAlaLysGluArgVa
Db   4331 CAGCACCACCAGCTTAACGGCGAGCGCGGGACCTCAGAGTGCCAAGGAGAGGG

Qy   380 TrpThrProCysGlyProHisGlnGlyGlnAspGlyArgGlyProAlaPr
Db   4391 TGGACCCCTGCGACCCACCAGGGCACCAGGATGAAGGGCGGGGCCAGCCCC

Qy   400 GlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThr--
Db   4451 GGCACCCGCCAGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGAACAGG

Qy   416 ---
Db   4511 CCCTCTGGGTGGGGAAGAGTGCTAGGTGGAGAGGAACTCAGCCCGAAGACAAA

Qy   417 -------------------AlaSerValAlaThrGlyProAspSerProS
Db   4571 ACAGGTGTTTTTTTCCTTCCCAGCTTCTTGTTGCCACCGGCCCAGACTTCCCCGT

Qy   429 lProLeuProProGlyProAlaLeuProGlyGlyAlaAspGlyThrProPheG
Db   4631 GCCTTTGCCCCCAGGCAAACCAGCCCTACCTGGGGCCGACGCGGACCCCCTTTG

Qy   449 o--
Db   4691 GTAAGTTGGGTATTGGAGACATGGGGGTGCTGCTCAGGTGTGTGGTACAGCC

Qy   450 ------------------------------------ProGlyArgLysGlul
Db   4751 CATCCGTGTTCACTGCTGTCTGTTTGTTTGATGCAGTCAGTCCGGGCGCCAAAGAG

Qy   457 erAspProValGluTrpThrValMetAspValValGluTyrPheThrGluAla
Db   4811 CTGATCCCGTCGAGTGGACCGTGATGGATGTGTCGAATATTTTACTGAGGCTC

Qy   477 roGluGluGlnAlaThrAlaPheGlnGlu--
Db   4871 CGGAGCAGGCAGCACAGCTTTCCAAGA-GCAGGTGAGTTTCAGCCCAGGACTACA

Qy   485 ---
Db   4930 CAGACACAGAGGGCCTCCCTGGGATGTGCCCATCCCGGCTTTCTCTGTTCCT

Qy   486 --GlnGluIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspValLeuT
Db   4990 CCCAGGAAATTGATGGCAAATCTTTGCTGCTCATGCAGCGCACAGATGTGCTCA

Qy   505 euSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLysValL
Db   5050 TGTCCATCCGCCTCGGGCCCAGCCCTGAAAATCTACGAGCACCACCATCAAGGTGC

Qy   525 lnGlyHisPheGluAspAspAspProAspGlyPheLeuGly 538
Db   5110 AAGGCCACTTTGAGGATGATGACCCCGATGGCTTCTTAGGC 5150

RESULT 11
US-09-976-740-48
; Sequence 48, Application US/09976740
; Publication No. US2002019463JA1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREA
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/976,740
; CURRENT FILING DATE: 2001-10-12

Db   3251 CCGCCGCCGCCGCCGCCCCGCCCCGCCCCCACGCGCCGCCACGCGCCCCGTC

Qy   160 laAlaAlaAlaAlaProAlaProAlaArgAlaAlaAlaAlaAlaAlaThrAlaPro
Db   3311 CCGCCGCCGCCCCGGCCCGGCGCCCCGGCGCCGCCCCGGCCCCACAGCGCCCCCC

Qy   180 erProGlyProAlaGlnProGlyProAlaGlnArgAlaGlnArgAlaAlaProAlaPro
Db   3371 CGCCTGGCCCCGCGCCAGCCCGCCCCCGGCGCCCGGGCCGGCCCCCTGCGCGCCGG

Qy   200 roProAlaProAlaAlaProProAlaValAlaProAlaGlyProAlaArgAlaAlaPro
Db   3431 CGCCCGCGCCAGCCGCTGCCCCCGGCGTGGCCCCCGCCCGGCCCGCCGCGCCCCCC

Qy   220 roProAlaValAlaAlaAlaArgGluProProProGlnProProAlaPro
Db   3491 CGCCCGCCGTCGCCCCCGGAGCCGCCGCCGCCGCCCCACAGCCCCGGCCGCCG

Qy   240 oGlnGlnGlnGlnProProProGlnProProProGluGlyGlyGlyAlaVal
Db   3551 ACAGCAGCAGCCGCCCCCGCCCCAGCCGCCGCCGGAGGGGGGCCGCGGTG

Qy   260 gAlaGlyGlyGlyAlaAlaAlaArgProValSerLeuArgGluValValArgTyrLeuGlyGly
Db   3611 GGCCGGCCGGCGGCGCGGCCGGTGAGCCTGCGGGAAGTCGTGCGCTACCTCGGGGGC

Qy   280 rGlyGlyAlaAlaGlyGlyGlyArgLeuThrArgGlyArgValGlnGlnGluLeuLeuGluGluGlu
Db   3671 CGGCGGGGCGCGGGCCGGCGTCGCCTAACCCGCGCGCGCGGGGGCTGCGGGAGGAGGAG

Qy   300 aAlaAlaArgGlyLeuGluLeuAlaThrArgLeuGlyLeuAlaLeuProProGlyArgGly
Db   3731 GGCGGCTTCGAGGCGTCTGGAGCGCACCGTCTCGGAGCGCGCTTGCGCTGCCCCGCGGG

Qy   316 pArgProGlyArgGlyAlaProProAlaAlaSerAlaArgProSerArg-------
Db   3791 CAGGCCCCGACCGGGCGCGCGCCGCCCGCCCCCGTCTCGCAGCAAGGTGAGC

Qy   316 ---
Db   3851 BCCGGGGAGCGCGGGGCGCCGCCGGTGGGCCAGGTGCCGGCGAAGTTGGTGGCGGGGGC

Qy   316 ---
Db   3911 BAGTCCCGGGAGGAGGAACTGGGGTGGCGGGTGGCTTTGCGCGCGCTTTCCTGCGGGG

Qy   316 ---SerLysArg 319
Db   3971 GGTGCGTGGTGACCTTGGCAAGTGATTGAATCTCCCGGAGCCTCAGTTTCCTCCGCT

Qy   319 ---AGA 4210
Db   4151 CGTATTGTTCTTAAAGGTGGAATCGGTTCCTCCTCCCCACCGCCCGGACGCCCACAGT

Qy   339 GlyGluGluArgValLeuGluLysGlyLeuGluGluAspAspAspGluAspGluAsp
Db   4270 GGTCTGGGATTAGAACAGCTACTAATTTGCATGCTTCTCTCCGGCTCCAG-AGA
             GGAGAAGAGCCGAGTACTTGAGAAAGAAGAAGAAGATGATGAAGATGAAGAT

Qy   359 GluAspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyValAla
Db   GGTTGTGTCGAGGGCTTTAGTGAGTTAACACAGAGCCTGCACGGAGAGTGAATGCGTAAAAGTTA

TION NUMBER: 09/616,289
DATE: 2000-07-14
TION NUMBER: US 08/979,608
DATE: 1997-11-26
TION NUMBER: US 60/031,930
DATE: 1996-11-27
TION NUMBER: US 60/048,547
DATE: 1997-06-03
ID NOS: 53
:SEQ for Windows Version 4.0

rctolagus cuniculus

6)...(1895)

```
        3.48e-130        Length:        2561
        2594.00          Matches:       503
y:      94.20%           Conservative:  17
rity:   91.12%           Mismatches:    16
        91.02%           Indels:        16
        9                Gaps:          8
```

(1-538) x US-09-976-740-48 (1-2561)

```
        AlaGlyProAlaLeuProProProGluThrAlaAlaAlaThrThr---Ala  19
Qy  215 ProGlnProProAlaProProGlnGlnGln-----------ProPro
        ||||||||||||||||||||||||||||||||||||||  |  ||
        GCGGGGGCCCCCGGCCCTACCCCGCCGGAGAGCGGCCACCACACGGCCGCG  305
Db  900 CCACAGCGCCGGCGCCCGCCACAGCAGCAGCAGCAGCGCCGCCGCCACCGCCG
```

```
        AlaAlaSerSerSerAlaAlaSerProHisTyrGlnGluTrpIleLeuAspThrIle  39
Qy  230 GlnProGlnProProGluGlyAlaValArgAlaGlyGlyAlaAlaArg
        ||||||||||||||||||||||||||||||||||||||||||  |||||
        GCCGCCTCGTCTCCGCCGCTTCCCCGACTACCAAGAGTGGATTCTGGACACCATC  365
Db  960 CAGCCACAGCCGCCGCCGGAGGGCGCGGGCGCGGCGGGCCCGGCGCGGG
```

```
        SerLeuArgSerArgLysAlaArgProAlaSerpLeuGluArgIleCysArgMetValArg  59
Qy  250 SerLeuArgGluValValArgTyrLeuGlyGlySerGlyGlyAlaGlyGlyGlyArg
        ||||||||||||||||||||||||||||||||||||||||  ||||||
        TCGCTGCGCTCGCGCAAGGCGCGCGCCGGACCTGGAGCGCATCTGCCCGGATGGTGCGG  425
Db 1020 AGCCTGCGGGAAGTCGTGCGCTACCTCGGGGGTAGCAGCGGCGCTGGCGGCCGC
```

```
        ArgHisGlyProGluProGluArgThrArgAlaAlaGlaGluLeuLysLeuIleGlnGln  79
Qy  270 ArgGlyArgValGlnGlyValLeuLeuGluGluGluAlaAlaArgGlyArgLeu
        |||||||||||||||||||||||||||||||||||| ||  :||||
        CGGCACGGGCCGGAGCCGGAGCGCACGCGCGCCGAGCTCGAGAAACTGATCCAGCAG  485
Db 1080 CGGCGGCCGCGTGCAGGGGTCTGCTTGGTGGAAGAGGAGGCGGCGGGGCCGCCCTG
```

```
        AlaValLeuArgValSerTyrLysGlySerIleSerTyrArgAsnAlaAlaArgVal  99
Qy  290 ThrArgLeuGlyAlaLeuAlaLeuProArgGlyAlaAspArgProGlyArgAlaPro
        ||||||||||||||||||||||||||||||||||||||  ||||  ||
        SCCGTGCTCCGGGTCAGCTACAAGGGGAGCATCTCGTACCGCAACGCGGCGCGGGTC  545
Db 1140 ACCCGTCTCCGAGCGCTTGGCGTGCCCCGGGACAGGCCCGGCGCGGGCGCCA
```

```
        ProProAlaAlaArgGlyAlaThrProProAlaProProArgGlyAlaProArgGlyAlaPro  119
Qy  310 AlaSerAlaArgProSerArgLysArgGlyGlyGluGlyValLeuGlu
        ||||||||||||||||||||||||||||||||||||||||||
        CCGCCCGGCGGCGGAGCCACCCCGCCCGCGCCCCCCGGCGGGGCCCC  605
Db 1200 GCCAGCGCCCGCCCGGGACCAAAGAGAGAGCTGGGCGGAGGAGGCAGAGTCTTGAA
```

```
        AlaAlaAlaAlaAlaAlaProProThrProAlaProProAlaProProAlaPro  139
Qy  330 GluGluGluAspAspAspGluAspGluGluAspAsp------ValSer
        |||||||||||||||||||||||||||||||  ::::::   ||
        --GCCGCCCGGCGGCGGCGCCCCCCGCGCCCCGCGCCGCCGCGCCGCCC  659
Db 1260 GAGGAGGAGGAGGAGGAGGACGACGAGACGACGAGACGACGACGTCGTGTCCC
```

```
        --AlaAlaAlaAlaProAlaArgAlaProArg-----AlaAlaAlaAlaAlaAla  156
Qy  348 SerGluValProGluSerAspArgProGlyAlaGlyAlaGlnHisHisGlnLeuAsn
        ||||||||||||||||||||||||||||||||||||||||
        SCCGCCCGGCGGCGGCCCGGCCCGGGCCCCGCCCGCGCGCCCGGCCCGCCGCCCG  719
Db 1320 TCGGAGGTGCCCGAGAGCGATCGTCCCGGGGTGGCGGCGCAGCATCACCAGCTGAATC
```

```
        AlaProSerProGlyProAlaGlnProGlyProArgAlaGlnArgAlaAlaAlaPro  176
Qy  367 GluArgGlyProGlnSerAlaLysGluArgValLysGluGlyTrpThrProCysGlyI
        ||||||||||||||||||||||||||||||||  ::::||
        SCGCCCCCTCGCCCGCCAGCCGGGCGCCCCCCGCGCGGGGGCGGCCCG  779
Db 1380 GAGCGCGGGCCCCGCCAGACGGCCAAGGAGCGGGTCAAAGAGTGTCGGCTGTGTGCC
```

```
        AlaAlaProProAlaProProAlaAlaProProAlaValAlaProProAlaGlyProPro  196
Qy  387 GlnGlyGlnAspGlyArgGlyProAlaProGlySerGlyThrArgGlnValF
        |||||||||||||||||||||||||||||||::::||
        :CCGGCCCGCCGCCGCCCGCCGCTCCCCCCGGCCCGGCGCCCGCCG  839
Db 1440 CCTGCCCAGGAGAGGAGGGCGGGGCCCGCCGCAGTGGCACCCGCCAGGTGT
```

```
        rgAlaProPro-----AlaValAlaAlaArgGluProProLeuProProPro  214
Qy  407 MetAlaAlaMetAsnLysGluGlyValGlyValGlyThrAlaSerValAlaThrGlyProAspS
        ||||||||||||||||||||||||  |||||||||
        GCGCCCCCCCCGCCGCCGCCCGTCGCCCCGCCGCCCGGGAGTCGCCGCTCGCCGCCGCCG  899
Db 1500 ATGGCGGCCTTGAGTAAGGAGGGGGATCAGCCTCTTCGACCACCCGGGCCCTGACT
```

```
Qy  427 SerProValProLeuProProGlyLysProAlaLeuProGlyLysAlaAspGlyThrP
        ||||||||||||||||||||||||||||::::||
Db 1560 TCCCGGTGCCTTTGCCCCCCCGGGAGCCCAGCCCCTCCCAGAGACCGATGGGACCC
```

```
Qy  447 GlyCysProProGlyArgGlyGluLysProSerAspProValGluTrpThrValM
        ||||||||||  :::||
Db 1620 GGCTGCCCTGCCGGGGCCAAAGGAAGGCCGGCAGACCCCGTGGAGTGGACAGTCA
```

```
Qy  467 ValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThrAlaPheGlnG
        ||||||||||||::::|||
Db 1680 GTCGTGGAGTACTTCACCGAGGCGGGCTTCCCTGAGCAAGCCACGGCTTTCCAGG
```

```
Qy  487 GluIleAspGlyLysSerLeuLeuMetGlnArgThrAspValLeuThrGlyLu
        ||||||||||||::::|||
Db 1740 GAGATCGACGGCAAGTCCCTGCTCTGCTCATGCAGCGCACCGATGTCCTCACCGGCC
```

```
Qy  507 IleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLysValLeuGlnG
        ||||||||||||||||||
Db 1800 ATCCGCTCTGGGGCCAGCGTTGAAAATCTATGAGCATCACCATATCAAGGTGCTGCAGCG
```

```
Qy  527 HisPheGluAspAspAspProAspGlyPheLeuGly  538
        |||||||::::|||
Db 1860 CACTTCGAGGACCATGACCCCGAAGGCTTCCTGGGA  1895
```

RESULT 12
US-10-671-242-48
; Sequence 48, Application US/10671242
; Publication No. US20040040049A1
; GENERAL INFORMATION:

ees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
ENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
ENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
ENTION: ATHEROSCLEROSIS
CE: 10797-004001
ICATION NUMBER: US/10/671,242
NG DATE: 2003-09-24
ATION NUMBER: US/09/616,289
  DATE: 2000-07-14
ATION NUMBER: US 09/517,849
  DATE: 2000-03-02
ATION NUMBER: US 08/979,608
  DATE: 1997-11-26
ATION NUMBER: US 60/031,930
  DATE: 1996-11-27
ATION NUMBER: US 60/048,547
  DATE: 1997-06-03
) ID NOS: 53
tSEQ for Windows Version 4.0

yctolagus cuniculus
s
46)...(1895)

:
        3.48e-130   Length: 2561
        2594.00   Matches: 503
ty: 94.20%   Conservative: 17
arity: 91.12%   Mismatches: 16
        91.02%   Indels: 16
        12   Gaps: 8

(1-538) x US-10-671-242-48 (1-2561)

```
157  Qy  ThrAlaProSerProGlyProAlaGlnProGlyProArgAlaGlnArgA
         ||||||||||||||||||||||||||||||||||||||||||||
720  Db  ACAGGCCCCCTCGCCCCGGCCCCGCAGCCCGGCGGGCCCCGCGGCCAGCGGG

177  Qy  LeuAlaAlaProProProAlaProAlaAlaProProAlaAlaProProA
         ||||||||||||||||||||||||||||||||||||
780  Db  CTGGCCGCGGCGCCGCCCCCGGCCCCGCTCCCCCGCGGCGGGCCCCCCGGC

197  Qy  ArgArgAlaProPro-----AlaValAlaAlaArgGluProProLeuPr
         |||||||||||            ||||||||||||||||||||
840  Db  CGCCGCGGCCCCCGCCCGCGGCCGTCGCCGCCCGGGAGTCCCGCCTGCC

215  Qy  ProGlnProProAlaProProGlnGlnGln------------ProPr
         ||||||||||||||||||||||||              ||
900  Db  CCACAGCCGCCGGCCGCCACAGCAGCAGCAGCCGCCGCCGCCACCGCC

230  Qy  GlnProGlnProProGlyGluGlnProGlyGlyAlaGlyAlaValArgGl
         |||||||||||||||||||||||||||  |||||||
960  Db  CAGCCACAGCCGCCGCCGCCGGAGGGGGCCCGGCGGCCGCCGCCGGCCG

250  Qy  SerLeuArgGluValValArgTyrLeuGlyLySerGlyGlyAlaGlyAr
         ||||||||||||||||||||||||||||||||
1020 Db  AGCCTGCGGGAAGTCGTGCGCTACCTCGGGGGTAGCAGCGGCCCTGGGCGGCCG

270  Qy  ArgGlyArgValGlnGlyValGluGluLeuGluGlyAlaGlnArgGlyArgGle
         ||||||||||||||||||||||||||||
1080 Db  CGCGGCCGGCGTGCAGGGCGTCTGCTGGAAGAGGAAGCCGGCGGGCGGGGCGCC(

290  Qy  ThrArgLeuGlyAlaLeuAlaLeuProArgGlyArgAspArgProGlyArgAlaPr
         ||||||||||||||||||||||||||||||||
1140 Db  ACCCGTCTCGGAGCGCGTTGCGCTGCCCCGCGGGGACAGGCCCGAGGACGGGCGCC)

310  Qy  AlaSerAlaAlaArgProSerArgSerlyGlyGluGlyValLeuGl
         |||||||||||     ::::|||::::|||||||||
1200 Db  GCCAGCGCGCCCGGCGCGGCGACCGCCGAACAAGAAGAAGCTGGCGGAGGAGCGCGCGTTGA

330  Qy  GluGluGluAspAspAspAspAspGluGluAspAsp------ValSer
         ||::::::||||::::||::::||::::::::::
1260 Db  GAGGAGGAGGAGGAGGAAGACGACGAGGACGACGACGTCGTGTCC

348  Qy  SerGluValProGluSerAspArgProAlaGlyAlaGlnHisHisGlnLeuAsn
         |||||||||||||||||||||||||||||||
1320 Db  TCGGAGGTGCCCGAGAGCGATCGTCCCGGGGTGCGCAGCATCACCAGGTGAAT

367  Qy  GluArgGlyProGlnSerArgAlaLysGluLysProThrProCysGly
         |||||||||||   ::::::|||::::|||
1380 Db  GAGCGCGGCCCGCAGACCGCCAAGGAGCGGCCAAGGAGTGGTCGCGTGTGGC

387  Qy  GlnGlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThrArgGlnVal
         ||::::|||   ::::||||||||||||||||
1440 Db  CCTGGCCAGGAGGAAGGCGGGCCGGGCAGGTGGCCACCCCGCCAGGTG

407  Qy  MetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThrGlyProAsp:
         |||||||||||    ::::::|||||||||||||
1500 Db  ATGGCGGCCTTGAATAAGGAGGGGGATCAGCCTCTTCGACCACCGGGCCTGAC

427  Qy  SerProValProLeuProProGlyLysProAlaLeuProGlyAlaAspGlyThr:
         ||||||||||   ::::::|||||||||||||
1560 Db  TCCCCGGTGCCTTTGCCCCCGGGAAGCCAGCCCTCCCAGAGGCCGATGGGACCC

447  Qy  GlyCysProProGlyArgLysProLysProSerAspArgProValGluTrpTrpProCysGly\
         |||||||||||    ::::::|||||||||||||
1620 Db  GGCTGCCCTGCCCGGCGCCAAAGAGAGGAGGGCGCGCAGACCCCGTGGAGTGGACAGTCA\

467  Qy  ValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThrAlaPheGlnG
         |||||||||||||||||||||||||||||
1680 Db  GTCGTGGAGTACTTCACCGAGGCGGGCTTCCCTGAGCAAGCCACCGGCTTTCCAGG

487  Qy  GluIleAspGlyLysSerLeuLeuMetGlnArgThrAspValLeuThrGlyL
         |||||||||||||||||||||||||||||||
1740 Db  GAGATCGACGGCAAGTCCCTGCTCATGCAGCGCACCGATGTCCTCACCGGCC

507  Qy  IleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLysLysValLeuGluGlnG
```

```
:AlaGlyProProAlaLeuProProProGluThrAlaAlaAlaAlaThrThr---Ala  19
 ||||||||||   |||    |||||||||||||||                |||
GCGGGGCCCCCGGCCCTCACCCCCGCCGAGACGGCGGCCGCCGCCACCGGCGCCG  305

:AlaAlaSerSerSetAlaAlaSerProHisTyrGlnGluTrpGlnGluTrpIleLeuAspThrIle  39
 |||||||||||||||||||||||||||||||||||
:GCCGCCTCGTCCGCCGCTTCCCCGACTACCAAGAGTGGATTCTGGACACCATC  365

:SerLeuArgSerArgLysAlaArgProAspLeuArgIleCysArgMetValArg  59
 ||||||||||||||||||||||||||||||||||||
:TCGCTGCGCTCGCGCAAGGCGCGGCCCGACCTGGAGCCGCCATCTGCCGGATGGTGCGG  425

:ArgHisGlyProGluProGlyArgThrArgAlaLeuGluleuGluLysLeuGlnGln  79
 ||||||||||||||||||||||||||||||||||
:CGGCACGGCCCCGAGCCCGGACGCACGCGCGCCCTCGAGCTCGAGAAACTGCAGCAG  485

:AlaValLeuArgValSerTyrLysGlySerIleSerTyrArgAsnAlaAlaArgVal  99
 |||||||||||||||||||||||||||||||||||
:GCGGTGCTTCCGGGTCAGCTACAAGGGGAGCATCTCGTACCGCAACGCGGCGCCGTC  545

:ProProGlyArgGlyAlaThrProAlaProProAlaProArgGlyAlaProGlyAlaPro  119
 ||||||||||||||||||||||||||||||||||
:CCGCCCCGGCGCGGAGCCACCCCCGCGCCCCCGGCCCCGCGCGGGGGCCCC  605

:AlaAlaAlaAlaAlaProProProThrProAlaProProProProProAlaPro  139
 |||||||||||||||||||||||||||||||
---GCCGCCGCGGCCGCGCCGCCCCACGCCCCGGCCCCGCGCGGGCCGCGCCC  659

:---AlaAlaAlaAlaProAlaArgAlaProAlaProArg------AlaAlaAlaAlaAlaAla  156
 |||||||||||||||||||||||||||||||
:GCCGCCGCCGCCGCCGGGGCGCCCGGCGCCCCCGCGCGGGCCGCCGCTGCCGCC  719
```

```
                                                                                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                                                                    CCGCCTGGGGCCAGCGTTGAAAATCTATGAGCACCATATCAAGGTGCTGCAGCAGGGT 1859

                                                                             sPheGluAspAspProAspGlyPheLeuGlY 538
                                                                             |||||||||||||||||||:::||||
                                                                             CTTCGAGGACGATGACCCGGAAGGCTTCCTGGGA 1895

                                                              pplication US/10023529
                                                              .US20020129388A1
                                                         TION:
                                                         B, Ann M.
                                                         ees, Robert S.
                                                         w, Simon W.
                                                         jona, Anibal A.
                                                   TION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
                                                   TION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
                                                   TION: ATHEROSCLEROSIS
                                                   : 10797-004001
                                             CATION NUMBER: US/10/023,529
                                             G DATE: 2001-12-17
                                             ION NUMBER: 09/616,289
                                             DATE: 2000-07-14
                                             ION NUMBER: US 09/517,849
                                             DATE: 2000-03-02
                                             ION NUMBER: US 08/979,608
                                             DATE: 1997-11-26
                                             ION NUMBER: US 60/031,930
                                             DATE: 1996-11-27
                                             ION NUMBER: US 60/048,547
                                             DATE: 1997-06-03
                                             ID NOS: 53
                                             SEQ for Windows Version 4.0

                                   ctolagus cuniculus

                             6)...(1895)

                             3.48e-130        Length:        2561
                             2594.00          Matches:       503
                        y:   94.20%           Conservative:  17
                        rity: 91.12%          Mismatches:    16
                             91.02%           Indels:        16
                             13               Gaps:          8

                  (1-538) x US-10-023-529-48  (1-2561)

             AlaGlyProAlaLeuProProGluThrAlaAlaAlaAlaThr---Ala 19
             |||||||||||||||||||||||          |||||
             GCGGGGGCCCCCGCGCCCTACCCGGAGACGACGGCCGCCACCGCCGCG 305

        AlaAlaSerSerAlaAlaSerProHisTyrGlnGluTrpIleLeuAspThrIle 39
        |||||||||||||||||||||||||||||||||:::||||
        GCCGCCTCGTCGTCCCCGCGCTTCCCCGCACTACCAAGAGTGGATTCTGGACACCATC 365

     SerLeuArgSerArgLysAlaArgProAspLeuUArgIleCysArgMetValArg 59
     |||||||||||||||||||||||||||||||||:::||||
     TCGGCTGCGCTCGCGCAAGGCCGGCCGGCCGGACCTGAGCGCATCTGCCGGATGGTGCGG 425

   ArgHisGlyProGluProGluThrArgAlaGluLeuGluLysGluLeuGlnGln 79
   |||||||||||||||||||||||||||||||||:::||||
   CGGCACGGGCCGGAGCCGGAGACGCGCACGCGCCGGAGCTCGAGAAACTGATCCAGCAG 485

 AlaValLeuArgValSerTyrLysGlySerIleSerTyrArgAsnAlaAlaArgVal 99
 |||||||||||||||||||||||||||||||||:::||||
 GCCGTGCTCCCGGGTCAGCTACAAGGGGAGCATCTGTACCGGCAACGGCGGCGCCGTC 545
```

```
Qy  100  GlnProProArgArgGlyAlaAlaThrProProAlaProProArgAlaProArgGly
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  546  CAGCCGCCCCGGCGCGGAGCCACCCGGCCACCCCGCGCGCCCCCGCGCCCCCCGGGG

Qy  120  AlaAlaAlaAlaAlaAlaAlaAlaProProProThrProAlaProProProPro
         ||||||||||||||||||
Db  606  ------GCCGCCGCGCCGCCGCGCCCCCCAGCCCCGCCGCCGCGCCGCCCCCCC

Qy  140  Val---AlaAlaAlaAlaProAlaAlaArgAlaProArg-----AlaAlaAlaAla
         |||        ||||||
Db  660  GTGCCGCGCGCCGCGCCCCCGGCGCCGGCGCCGCGCCGGCGGCCGGCCGCGCCGCT

Qy  157  ThrAlaProProSerProGlyProAlaGlnProGlyProArgAlaGlnAlaArgAla
         |||||||||||||||||||||||||||
Db  720  ACAGCGCCCCCCTCGCCCGGCCCCGCCCAGCCCGGCCCGCGCAGGCGCAGGCGCGGGCC

Qy  177  LeuAlaAlaProProGluProAlaAlaProProAlaProProAlaValAlaProProAla
         |||||||||||||||||||||||||||||||||
Db  780  CTGGCCGCGCCGCCGGAGCCCGCCGCTCCCCCGGCGCCGCCGGCGGCGCCCCCGGCC

Qy  197  ArgArgAlaProProPro------AlaValAlaAlaArgGluProProLeuProl
         |||||||||
Db  840  CGCCGCGCCCCCCGCCCCGCCGCCGCGCTGCCGGCCGCCCGGAGTCGCCCGCTGCCGC

Qy  215  ProGlnProProAlaProProGlnGlnGln------------------ProPro
         ||||||
Db  900  CCACAGCCGCCGGCCGCGCCCCAGCAGCAGCAGCAGCAGCCGCCACCGCCGCG

Qy  230  GlnProGlnProProGluGlyGlyValAlaValAlaArgAlaGlyGlyAlaAlaArgl
         |||||||||||||||||||||||||
Db  960  CAGCCACAGCCGCCGGAGGGGGGCGGCGCCGCGGGCGGGGCCCCGGGCGGGCCGCGCGG

Qy  250  SerLeuArgGluValValArgTyrLeuGlyLyGlySerGlyGlyAlaGlyGlyArgl
         ||||||||||||||||||
Db  1020 AGCCTGCGGGAAGTCGTGCGCTACCTCGGGGGTAGCAGCGGCGGCCTGCGCGCGCC

Qy  270  ArgGlyArgValGlnGlyLeuLeuGluGluGluAlaArgGlyArgLeuC
         ||||||||||||||||
Db  1080 CGCGGGCCGGTGCAGGGTCTGCTGGAAGAGGAGGCCCGGGGCCGGCCGCTGC

Qy  290  ThrArgLeuGlyAlaLeuAlaLeuProArgGlyAspArgArgProGlyArgAlaProl
         ||||||||||||||||||
Db  1140 ACCCGGTCTCGGAGCGGCTTGCGTGCCCGGGGACAGGGCCCGGACGGGGCGCCACC

Qy  310  AlaSerAlaArgProSerArgLysSerArgGlyGlyGluGluLysGluLeuGluL
         |||::||||:::||||
Db  1200 GCCAGCGCCGCCGGCGCGGCGAACAAGAGAGCTGGCGGAGAGCGGAGTGCTTGAAA

Qy  330  GluGluGluAspAspAspAspGluGluGluAspAsp-----ValSerG
         ||||:::::::::||||
Db  1260 GAGGAGGAGGAGGAGGAGGAAGACGACGACGACGAGCGTGTCCG

Qy  348  SerGluValProGluSerAspArgProAlaGlyAlaGlnHisHisGlnLeuAsn-
         ||||||||||||||||||
Db  1320 TCGGAGGTGCCGGAGAGCGATCGTCCCGGGGTGCGCAGCATCACCAGCTGAATG

Qy  367  GluArgGlyProGlnSerAlaLysGluArgValLysGluTrpProCysGlyP
         ||||:::||||
Db  1380 GAGCGCGGCCCGCAGAACCGCCAAGGAGCGGGCCAAGAGAGTGGTCGCTGGCC

Qy  387  GlnGlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThrArgGlnValPl
         |||:::||||
Db  1440 CCTGGCCAGGAGGAAGGGCCGGGCCGCCGCGGGCCAGTGGCACCCGCAGGTGT

Qy  407  MetAlaAlaMetAsnLysGluGlyThrAlaSerValAlaThrGlyProAspSe
         |||:::||||
Db  1500 ATGGCGGCCTTGACTAAGGAGGGGGATCAGCCCTTCACCACCGGGGCTGACT

Qy  427  SerProValProLeuProProGlyLysProAlaLeuProGlyAlaAspThrPl
         |||:::||||
Db  1560 TCCCCGGTGCCTTTGCCCCCGGGAAGCCAGCCCTCCAGGAGCCGATGGGACCCl

Qy  447  GlyCysProGlyArgLysProSerAspProValGluTrpThrValMe
```

```
Qy   40  AspSerLeuArgSerArgLysAlaAlaArgProAspLeuGluArgIleCysArgMe
         ||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db  366  GACTCGCTGCGCTCGCGGCAAAGAAGAGAGCGGCAGACCCCGTGGAGTGGACAGTCATCGGAT

Qy   60  ArgArgHisGlyProGluProGlnArgThrArgAlaGluLeuGluLysLeuI
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  426  CGGCGGCACGGCCCGGAGCGGCCAGCCACGCGCCGCCGAGCTCGAGAAACTGAT

Qy   80  ArgAlaValLeuArgValSerTyrLysGlySerIleSerTyrArgAsnAlaAl
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  486  CGCGCCCGTGCTCCGGGTCAGCTACAAGGGGAGCATTCTACCGCAACGGCGGC

Qy  100  GlnProProArgArgGlyAlaThrProProAlaProProArgAlaProArgGl
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  546  CAGCCGCCCGGCGCGGAGCCACCCCGGCCACCCCGGGCGCCCCGCCGCGCGGG

Qy  120  AlaAlaAlaAlaAlaAlaProProProThrAlaProProProProPr-----AlaAlaAlaAl
         |||||||||||||||||||||||||||||||||||||||||||||
Db  606  ------GCGGCCGCCGCCGCGCCGCCCGCCCCAGCCCCGCGCCCCGCCGCCGCC

Qy  140  Val---AlaAlaAlaAlaProAlaAraAlaAlaAraAla-----AlaAlaAlaAl
         ||                           ||||||||||
Db  660  GTCGCCGCGCCGCGCCGCCCCGGCCCCGGCCCCGCGCCGCGCCGCCGCCGCGC

Qy  157  ThrAlaProProSerProGlyProAlaGlnProGlyProArgProAlaGlnArgAl
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  720  ACAGGCCCCCTCGGCCCGGCCCCGGCGCAGCCGGGCCCGCGGCCAGCCGCGGC

Qy  177  LeuAlaAlaProProProAlaAlaProProAlaValAlaProProAl
         |||||||||||||||||||||||||||||||||||||||||||
Db  780  CTGGCCGCCCCGCCGCCCGCCGCTCCCCCGGCGGGCCCCCGCC

Qy  197  ArgArgAlaProProPro-----AlaValAlaAlaAlaArgGluProLeuPro
         ||||||||||||||||||||                     |||
Db  840  CGCCGGCGCCCCCCGCCCGCCGCCCGTGCGCCCCGGGAGTGCCGCCGCTGCCC

Qy  215  ProGlnProProAlaProProGlnGlnGln---------ProPro
         |||||||||||||||||||||||||||
Db  900  CCACAGCCGCCCGGCCGCCCCACAGCAGCAGCCGCCCCACCCGCC

Qy  230  GlnProGlnProProGlyGlyGlyAlaValArgAlaGlyGlyAlaAlaArg
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  960  CAGCCACAGCCGCCCGGAGGGGGGCGCGGGGCCGGCCCGGCGGCCCGGGCGG

Qy  250  SerLeuArgGluValValArgTyrLeuGlyTyrLeuGlyAlaAlaArgGlyTyrArg
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1020  AGCCTGCGGGAAGTCGTGCGCTACCTCGGGGGTAGCAGCGGCGCTGGCGGCCGC

Qy  270  ArgGlyArgValGlnGlyLeuLeuGluGluGluLeuAlaAlaArgGlyArgLeu
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1080  CGGGGCCGGGTGCAGGGGTTGCTGGAAGAGGAGGCGGCGGGGCGGGGGCCCTG

Qy  290  ThrArgLeuGlyAlaLeuAlaLeuProArgGlyAspArgProGlyAlaProPro------ValSer
         |||||||||||||||||||||||||||||||||||||||||     |||||
Db 1140  ACCCGTCTCGGAGCGCTTGCGCTCCCCCGCGGGGACAGGCCCGGACGCGGCCCA

Qy  310  AlaSerAlaArgProSerArgArgLysGlyGlyGluLeuArgValLeuGlu
         |||         :::|::::|||||||||:||||||||||||||
Db 1200  GCCAGCGCCCGGCCGGGAACAGGAGAGAGGTGGCGAGGAGCGAGTGCTTGAA

Qy  330  GluGluGluAspAspAspGluAspProAlaArgProGlyArgAlaPro-----ValSer
         |||||||||::::::::||||||||||||||||||||||
Db 1260  GAGGAGGAGGAGGAGGAGAACGACGAGGACGAGGACGACGAGGACGTCGTGTCCC

Qy  348  SerGluValProGluSerAspArgProAlaGlyProAlaGlyAlaGlnHisHisGlnLeuLeuAsn-
         ||||||||||||||||||||||||||||:::||||||:|||||||
Db 1320  TCGGAGGTGCCCGAGAGCGATCGTCCCGCGGGTGCCGCAGCATCACCAGCTGAATC

Qy  367  GluArgGlyGlyProGlnSerArgAlaLysGluArgValLysGluTrpProCysGlyTy
         |||||||||:::||||||||||||||||||||||||||||||||:::||||
Db 1380  GAGCGCGGCGGCCCGCAGAGCCGCAAGGAGCGGGTCAAGGAGTGGCCGTGTGGCC

Qy  387  GlnGlyGlnAsnGluAspGluGlyArgGlyProAlaProGlySerGlyThrArgGlnValI
```

```
ctolagus cuniculus

6)...(1895)


     3.48e-130     Length:        2561
     2594.00       Matches:       503
y:   94.20%        Conservative:  17
rity: 91.12%       Mismatches:    16
      91.02%       Indels:        16
      13           Gaps:          8

(1-538) x US-10-023-523-48 (1-2561)
```

```
||||||||||  ||||||     ||||||||||||||:::  ||||||||||||||||||||
GCTGCCCTGCGGGGCGCAAAGAAGAGAGCGGCAGACCCCGTGGAGTGGACAGTCATCGGAC  1679

alValGluTyrPheThrGlyAlaGlyIleProGluProGlnAlaThrAlaPheGlnGluGln  486
|||||||||||||||||||||||||||||||||||||||||||||||||||||||
CGTTGGAGTACTTCACCGGAGCGGGCTTCCCTGAGCAAGCCACGGCTTTCCAGGAGCAG  1739

uIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspValLeuThrArgGlyLeuSer  506
||||||||||||||||||||||||||||||||||||||||||||||||||||
GATCGACGGCAAGTCCCTGCTCATGCAGCGCACCGATGTCCTCACCCGGCCTGTCC  1799

eArgLeuGlyProAlaLeuLysIleTyrGluHisIleLeuLysValGlnGlnGly  526
|||||||||||||||||||:::|||||||||
CCGCTCGGGCCAGCGTTGAAAATCTATGAGCACCCATATCAAGGTGCTGCAGGGGT  1859

sPheGluAspAspAspProAspGlyPheLeuGlyGly  538
|||||||||||||||||
CTTCGAGGACGATGACCCGGAAGGCTTCCTGGGA  1895
```

```
AlaGlyProAlaLeuProProGluThrAlaAlaAlaAlaAlaThrThr---Ala  19
||||||||||||||||||||||||||||||||||||||         |||
GCCGGGCCCCCGGCCCTACCCCGCCGGAGACGGCGGCGCCACCACCGCCGCCG  305

AlaAlaSerSerSerAlaAlaSerProHisTyrGlnGluTrpIleLeuAspThrIle  39
|||||||||||||||||||||||||||||:::  |||
GCCGCCTCGTCGTCCGCGTCCCCGCACTACCAAGAGTGGATTCTGGACACCATC  365
```

DB:

US-09-976-740-43 (1-538) x US-10-616-187-48 (1-2561)

15   Gaps: 8

```
Qy      1  MetAlaGlyTyrProAlaLeuProProGluThrAlaAlaAlaAlaThrThr
Db    246  ATGGCGGGGCCCCGGCCCTACCCCCGCGGAGACGGCGGCGGCCACCACG

Qy     20  AlaAlaAlaAlaSerSerAlaAlaSerProHisTyrGlnGluTrpIleLeuAsp
Db    306  GCCGCCGCCTCGTCCGCCGCTTCCCCGCACTACCAAGAGTGGATTCTGGAC

Qy     40  AspSerLeuArgSerArgLyBAlaArgProAspLeuGluArgIleCysArgMet
Db    366  GACTCGCTGCGCTCCCGCAAGGCGGCCGACCTGGAGCGCATCTGCCGGATG

Qy     60  ArgArgHisGlyProGluProGluArgThrArgAlaCysAlaCGCGGCGGC
Db    426  CGGCGGCACGGCCCGGAGCCGGAGCGCACGCGCGCCTGCGCCGAGAAACTGATC

Qy     80  ArgAlaValLeuArgValSerTyrLysGlySerIleSerTyrArgAsnAlaAla
Db    486  CGGGCCGTGCTCCGGGTCAGCTACAAGGGAGCATCTCGTACCGCAACGGCGGC

Qy    100  GlnProProArgArgGlyAlaThrProProAlaProProArgAlaProArgGly
Db    546  CAGCCGCCCCGGCGCGGCGGAGCCACCCCGCCGGCGCCCCCGCGGGC

Qy    120  AlaAlaAlaAlaAlaAlaAlaProProThrProAlaProProProProPro
Db    606  GCCGCCGCGCGCGCCGCCCCACGCCCCGCGCCCCCGCCGCCCCCGCCGCCC

Qy    140  Val--AlaAlaAlaAlaProAlaArgAlaAlaProAlaArg-----AlaAlaAlaAlaAla
Db    660  GTCGCCGCCGCCCCCGGCCCCGGCCGCCCGGCGCCCGGCCCGGCCGTCGCCGCTC

Qy    157  ThrAlaProProSerProGlyProAlaGlnProGlyProArgAlaGlnArgAlaP
Db    720  ACAGCGCCCCCCTCGCCCGGGCCCGCGCAGCCGGGCCCGCGGGCCCAGCGGCGCCC

Qy    177  LeuAlaAlaAlaProProProAlaProAlaAlaAlaProProAlaValAlaProProAlaG
Db    780  CTGGCCGCGGCCCCGCCGGCCCCGGCCGCCCGTCCCCGGCGGCCCCCGCCC

Qy    197  ArgArgAlaProPro-----AlaValAlaAlaAlaArgGluProProLeuProF
Db    840  CGCCGCGCCCCCCGCGGCCGTCGGCCGCCCGGAGTCGCCGTGCCGC

Qy    215  ProGlnProProAlaProProGlnGlnGln----------------ProProP
Db    900  CCACAGCCGCCGGCGCCGCCACAGCAGCAGCCGCCGCCCCACCGCCCGC

Qy    230  GlnProGlnProProGluGlyGlyAlaValArgAlaGlyAlaAlaArgP
Db    960  CAGCCACAGCCGCCGGAGGGGCGGCGGCGCGGCCCCGGCCCGCGGCGGGC

Qy    250  SerLeuArgGluValValArgTyrLeuGlyLeuGluGluLeuAlaAlaAlaArgGlyArgLeuG
Db   1020  AGCCTGCGGGAAGTGGTGCGCTACCTCGGGGTAGCAGCCGCGCTGGGCGGCCGCC

Qy    270  ArgGlyArgValGlnGlyLeuLeuGluGluLeuAlaLeuAlaAlaAlaArgGlyArgLeuG
Db   1080  CGCGGCGCCGCGTGCAGGGTCTGCTGGAAGAGGAGGCGGCCGGGCCGGCCGGCCGCCTGG

Qy    290  ThrArgLeuGlyAlaLeuAlaLeuProArgGlyAspArgProGlyArgProAlaProP
Db   1140  ACCCGTCTCGGAGCGCTTGCGCTGCCCCGCGGGACAGGCCCGACGGCGGCCAC

Qy    310  AlaSerArgAlaArgProSerArgSerArgLyeArgGlyGlyValGluGluGluLuL
Db   1200  GCCAGCCGCGCCCGGCCGGCGGGACAAGAGAGCTGCGAGGAGGAGTGCTTGAAA

Qy    330  GluGluGluAspAspAspAspGluGluAspGluGluAspAsp------ValSerG
```

(right side of alignment — second block)

```
      |||||::::|||||              |||||||
   GGGCCAGGAGGAAGGGCGGGGGGCCCGCCGCAGTGGCACCCGCCAGTGTTCTCC  1499

AlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThrGlyTyrProAspSerPro  426
   |||||::::|||||
   GCCGGCCTTGAGTAGGAGGGGGGATCAGCCTCTTCGACCACCGGGCCTGGACTCCCCG  1559

ProValProLeuProProGlyLysProAlaLeuProGlyAlaAspGlyThrProPhe  446
   CCGGTGCCTTTGCCCCCGGGAGCCAGCCCTCCAGGAGCCGATGGGACCCCCTTT  1619

CysProProGlyTyrArgGlyGluLysProSerAspProValGluTrpThrValMetAsp  466
   TGCCCTGCCGGGCGCCAAAGAGAGCCGGCAGACCCCGTGGAGTGGACAGTCATGGAC  1679

ValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThrAlaPheGlnGluGln  486
   GTGGAGTACTTCACCGAGGCGGGGCTTCCCTGAGCAAGCCACGGCTTTCCAGGAGCAG  1739

IleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspValLeuThrGlyLeuSer  506
   ATCGACGGCAAGTCCCTGCTCATGCAGCGCACCGATGTCCTCACCGGCCTGTCC  1799

ArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLysValLeuGlnInGly  526
   CGCCTGGGCCCAGCGTTCAAAATCTATGAGCACCATATCAAGGTGCTGCAGCAGGGT  1859

PheGluGluAspAspAspProAspGlyPheLeuGly  538
   TTCGAGGACGATGACCCCGAAGGCTTCCTGGGGA  1895
```

plication US/10/616,187
US2004013668A1
TION:
s, Ann M.
es, Robert S.
w, Simon W.
jona, Anibal A.
TION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TION: ATHEROSCLEROSIS
: 10797-004001
ATION NUMBER: US/10/616,187
  DATE: 2003-07-09
ION NUMBER: US/09/616,289
ATE: 2000-07-14
ION NUMBER: US 09/517,849
ATE: 2000-03-02
ION NUMBER: US 08/979,608
ATE: 1997-11-26
ION NUMBER: US 60/031,930
ATE: 1996-11-27
ION NUMBER: US 60/048,547
ATE: 1997-06-03
ID NOS: 53
SEQ for Windows Version 4.0

ctolagus cuniculus

6)...(1895)

```
                    3.48e-130      Length:         2561
                   2594.00         Matches:         503
y:                  94.20%         Conservative:     17
rity:               91.12%         Mismatches:       16
                    91.02%         Indels:           16
```

---

5 09:28:16 2004

us-09-976-740-43.rnpb

```
||||||:::::::::::::::::::|||||||                        ||||||
AGGAGGAGGAGGAGGAGGACGACGAGACGACGACGAGCGTCGTGTCCGAGGGC  1319

rgGluValProGluSerAspArgProAlaGlyAlaGlnHisGlnLeuAsn--Gly  366
|||||:||||||||||||||||||||||||||||||||::||||  ||||||
CGGAGGTGCCCGAGAGCGATCGTCCCCGGGGTGCCGCAGCATCACCAGCTGAATGGCGGC  1379

LuArgGlyProGlnSerAlaLysGluArgValLysGluTrpProCysGlyProHis  386
|||||||||||::||||||||||||||  |||  ||||||||||||||
AGCCGCCGCCCCCAGACCGCCAAGGACGCGGGCCAAGGAGTGTCGCTGTGTGGCCCCCAC  1439

LnGlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThrArgGlnValPheSer  406
|||:::||||||||||||  |||||||||||||||||||||
TTGGCCAGGAGGAAGGGCGGGGGCCCGGCCCGGGCAGTGGCACCCGCCCAGGTGTTCTCC  1499

etAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThrGlyProAspSerPro  426
|||||||||||||||||||||||  ||||||||||||||||||
GGGCGGCCTTGAGTAAGGAGGGGGATCAGCCTCTTCGACCACCGGGCCTGACTCCCCG  1559

erProValProLeuProGlyLysProAlaLeuProGlyAlaAspGlyThrProPhe  446
||||||||||||||||||||||||||||||||||||||||
CCCGGTGCCTTTGCCCCCCGGGAAGCCAGCCCTCCCAGGAGCCGATGGGACCCCCTTT  1619

yCysProProGlyArgLysGluLysProSerAspProValGluTrpThrValMetAsp  466
|||||||||||||:::|||||||||||||||||||||||||||
CTGCCCCTGCCGGCGCCAAAGAGAGCCCGGCCAGACCCCCGTGGAGTGGACCAGTCATGGAC  1679

lValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThrAlaPheGlnGluGln  486
||||||||||||||||||||||||||||||||||||||||
CGTGGAGTACTTCACCGAGGCGGGCTTCCCTGAGCAAGCCACCGCTTTCCAGGAGCAG  1739

ulleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspValLeuThrGlyLeuSer  506
|||||||||||||||||||||||||||||||||||||||||||||
GATCGACGGCCAAGTCCCTGCTCATGCAGCGCACCGATGTCCTACCGGCCTGTCC  1799

eArgLeuGlyAlaAlaLeuLysIleTyrGluHisHisIleLysValLeuGlnGlnGly  526
|||||||||::::|||||||||||||||||||||||
CCGCCTGGGCCCAGCGTTGAAAATCTTATGAGCACCATATCAAGGTGCTGCAGCAGGGT  1859

sPheGluAspAspAspProAspGlyPheLeuGly  538
|||||||||:::||||||||
CTTCGAGGACGATGACCCCGGAAGGCTTCCTGGGA  1895
```

: March 13, 2004, 04:27:21
55 secs